GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: October 31, 2002, 19:48:26 ; Search time 251 Seconds
(without alignments)
13063.385 Million cell updates/sec

Title: US-09-919-197-3
Perfect score: 1456
Sequence: 1 tgagcaccagccaaccaggg.....tatgaaacactaaaaaaaaa 1456

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

number of hits satisfying chosen parameters: 2331924

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	45	3.1	65	24	ABN52223	Mouse spliced tran
c	2	31.4	2.2	49	18	AAT89492	CFTR binding site
c	3	27.8	1.9	60	24	ABN49410	Human spliced tran
c	4	27.6	1.9	47	21	AAZ66146	Human map-related
	5	26.2	1.8	47	21	AAZ65699	Human map-related
	6	26	1.8	73	21	AAA73834	Human HER2 partial
c	7	25.8	1.8	60	24	ABN40794	Human spliced tran
	8	25.4	1.7	47	22	AAH38784	Human SNP flanking
c	9	25.4	1.7	60	24	ABN39098	Human spliced tran
c	10	25.4	1.7	72	19	AAT97276	Nucleotide EP-13 S
c	11	25.2	1.7	65	24	ABN28389	Rat spliced transc
c	12	25	1.7	51	22	AAL30738	Human SNP oligonuc
	13	24.8	1.7	47	21	AAZ67790	Human map-related
	14	24.6	1.7	60	24	ABN47816	Human spliced tran
c	15	24.4	1.7	51	22	AAL30269	Human SNP oligonuc
	16	24	1.6	60	24	ABN39375	Human spliced tran
	17	24	1.6	65	24	ABN28030	Rat spliced transc
	18	23.8	1.6	64	21	AAA11650	Humanised anti-Fas
	19	23.8	1.6	64	24	ABL46029	Humanised anti-Fas
	20	23.8	1.6	75	9	AAN80654	75-mer probe used
c	21	23.6	1.6	47	21	AAZ66638	Human map-related
	22	23.6	1.6	50	22	AAL31451	Human SNP oligonuc
c	23	23.6	1.6	60	18	AAT61582	VH and scFv antibo
c	24	23.6	1.6	60	24	ABN32752	Human spliced tran
c	25	23.6	1.6	60	24	ABN32853	Human spliced tran
	26	23.6	1.6	60	24	ABN59247	Human spliced tran
c	27	23.6	1.6	71	18	AAT92616	SELEX-derived nucl
c	28	23.6	1.6	71	18	AAT78604	Class I SELEX gene
c	29	23.6	1.6	71	18	AAT59094	Human chorionic go
c	30	23	1.6	23	24	ABL45019	Human chromosome 1
c	31	23	1.6	51	22	AAL29070	Human SNP oligonuc
c	32	23	1.6	60	21	AAC23790	Human secreted pro
	33	22.6	1.6	50	22	AAH89731	Human coding sequ
	34	22.6	1.6	60	24	ABN32873	Human spliced tran
	35	22.6	1.6	60	24	ABN34691	Human spliced tran
	36	22.6	1.6	64	22	AAF80440	5-enolpyruvylshiki
	37	22.6	1.6	69	15	AAQ44415	Special AT-rich (A
	38	22.4	1.5	50	22	AAH89839	Human coding sequ
c	39	22.4	1.5	60	24	ABN44442	Human spliced tran
	40	22.4	1.5	68	22	AAL02305	Human reproductive
	41	22.2	1.5	43	21	AAA75934	PCR primer used to
	42	22.2	1.5	48	22	AAH22252	Anti-A33 antigen a
	43	22.2	1.5	48	22	AAH20117	Rabbit anti A33 an
	44	22.2	1.5	55	19	AAV70103	Humanised HFE7A he
c	45	22.2	1.5	55	20	AAX01319	Allelic ladder, HU

ALIGNMENTS

RESULT 1
ABN52223
ID ABN52223 standard; DNA; 65 BP.
XX
AC ABN52223;
XX
DT 15-JUL-2002 (first entry)
XX
DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:24971.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Mus musculus.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of

PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes -
XX
PS Example 1; SEQ ID 24971; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 65 BP; 15 A; 18 C; 14 G; 18 T; 0 other;

Query Match 3.1%; Score 45; DB 24; Length 65;
Best Local Similarity 83.6%; Pred. No. 0.004;
Matches 51; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```
Qy   1017 GACCTCTTCTTTCGCCCTATCATTGGAGATGTTGACATCGCTGGCCTTCTTGGGGACATG 1076
          || |||||||| |||||||||| ||||| ||||||||| ||| || |||| ||||||
Db      5 GATCTCTTCTTCCGCCCTATCATGGGAGACGTTGACATCACTGAACTCCTTGAAGACATG 64

Qy   1077 C 1077
          |
Db     65 C 65
```

RESULT 2
AAT89492/c
AAT89492 standard; DNA; 49 BP.
XX
AC AAT89492;
XX
DT 14-APR-1998 (first entry)
XX
DE CFTR binding site fragment 3.
XX
KW Cystic fibrosis transmembrane conductance regulator; CFTR; gene therapy;
KW protein binding site; nuclear extract; gene promoter; cystic fibrosis;
KW spatial expression regulator; CF; ss.
XX
OS Homo sapiens.
XX
PN WO9735005-A2.
XX
PD 25-SEP-1997.
XX
PF 20-MAR-1997; 97WO-GB00787.
XX
PR 20-MAR-1996; 96GB-0005808.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Harris A;
XX
DR WPI; 1997-480211/44.
XX
PT New oligo:nucleotide(s) for gene therapy of cystic fibrosis - are
PT able to increase the activity of the CF trans-membrane conductance
PT regulator gene promoter
XX
PS Claim 3; Page 16; 20pp; English.
XX
CC This sequence represents a minimum sequence required for binding of
CC proteins found in the nuclear extracts of cystic fibrosis transmembrane
CC conductance regulator (CFTR)-expressing cells. This sequence is an
CC oligonucleotide of the invention. This sequence, and sequences containing
CC it increase the activity of the CFTR gene promoter, so regulate spatial
CC expression of this gene (unlike viral or other promoters used in gene
CC therapy). Constructs containing this sequence are used in gene therapy of
CC cystic fibrosis (CF).
XX
SQ Sequence 49 BP; 15 A; 10 C; 5 G; 19 T; 0 other;

Query Match 2.2%; Score 31.4; DB 18; Length 49;
Best Local Similarity 77.6%; Pred. No. 32;
Matches 38; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy    557 AAGTGACTTGCCCAAGGTCACCCAGCTAATAAGTGACAGTGCTGGGATT 605
          |||| | ||||| ||| |||| | ||||||||||||| | | |||||
Db     49 AAGTAAATTGCCTAAGATCACATTGTTAATAAGTGACAGAGTTAGGATT 1
```

RESULT 3
ABN49410/c
ID ABN49410 standard; DNA; 60 BP.
XX
AC ABN49410;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:22158.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes -
XX
PS Example 1; SEQ ID 22158; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a

CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 60 BP; 10 A; 14 C; 16 G; 20 T; 0 other;

Query Match 1.9%; Score 27.8; DB 24; Length 60;
Best Local Similarity 69.1%; Pred. No. 4e+02;
Matches 38; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 563 CTTGCCCAAGGTCACCCAGCTAATAAGTGACAGTGCTGGGATTCATACCCAGGAA 617
||||||| || || | ||| || ||| |||| ||| ||||| |||| || |
Db 60 CTTGCCAGAGCTCTCAGAGCCAAAAAGCAACAGATGTGGAATTCAAACCCGGGCA 6

RESULT 4
AAZ66146/c
ID AAZ66146 standard; DNA; 47 BP.
XX
AC AAZ66146;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human map-related biallelic marker SEQ ID NO:493.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(24,G)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB00822.
XX
PR 21-APR-1998; 98US-0082614.
PR 23-NOV-1998; 98US-0109732.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome -
XX
PS Claim 1; Page 335; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 47 BP; 15 A; 9 C; 11 G; 12 T; 0 other;

Query Match 1.9%; Score 27.6; DB 21; Length 47;
Best Local Similarity 78.6%; Pred. No. 4e+02;
Matches 33; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 554 ATTAAGTGACTTGCCCAAGGTCACCCAGCTAATAAGTGACAG 595
||||||| |||||||||||||||| || || ||||| | |
Db 47 ATTAAGTCACTTGCCCAAGGTCATCCCCTTATTAAGTAGCTG 6

RESULT 5
AAZ65699
ID AAZ65699 standard; DNA; 47 BP.
XX
AC AAZ65699;
XX
DT 11-SEP-2001 (first entry)
XX
DE Human map-related biallelic marker SEQ ID NO:46.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(24,C)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB00822.
XX
PR 21-APR-1998; 98US-0082614.
PR 23-NOV-1998; 98US-0109732.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome -
XX
PS Claim 1; Page 240; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and

```
CC   haplotyping studies which are useful in determining the genetic basis
CC   for disease states. Compositions and methods of the invention can also
CC   be useful for the identification of the targets for the development of
CC   pharmaceutical agents and diagnostic methods, as well as the
CC   characterisation of the differential efficacious responses to and side
CC   effects from pharmaceutical agents acting on a disease as well as other
CC   treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC   and 3367, are not actually given a sequence in the Sequence Listing
CC   from the present invention.
XX
SQ   Sequence 47 BP; 17 A; 10 C; 11 G; 9 T; 0 other;

  Query Match             1.8%;  Score 26.2;  DB 21;  Length 47;
  Best Local Similarity   79.5%;  Pred. No. 1e+03;
  Matches   31;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy     550 AGAGATTAAGTGACTTGCCCAAGGTCACCCAGCTAATAA 588
           ||||||| |||||||   |||||||| |||||  | |||
         9 AGAGATTGAGTGACTAATCCAAGGTCTCCCAGGAATTAA 47


RESULT 6
AAA73834
ID   AAA73834 standard; DNA; 73 BP.
XX
AC   AAA73834;
XX
DT   15-FEB-2001  (first entry)
XX
DE   Human HER2 partial coding sequence #1.
XX
KW   Human; chorionic gonadotrophin; hCG; DNA vaccine; cancer;
KW   fertility control; contraceptive; immunogen; her2; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..2
FT                   /*tag=  a
FT                   /label= sticky_end
FT                   /note= "Also, the 5' end of the complementary strand
FT                   overhangs the 3' end of this strand by the sequence
FT                   5'-AA-3'"
FT   CDS             4..72
FT                   /*tag=  b
FT                   /product= "HER2"
FT                   /partial

PN   WO200041717-A2.
XX
PD   20-JUL-2000.
XX
PF   17-DEC-1999;   99WO-US30232.
XX
PR   18-DEC-1998;   98US-0112910.
XX
PA   (AVIB-) AVI BIOPHARMA INC.
XX
PI   Iversen PL;
XX
DR   WPI; 2000-466124/40.
DR   P-PSDB; AAB15359.
XX
PT   Inducing immune response to human chorionic gonadotropin (hCG), useful
PT   for treatment of cancer and fertility control comprises exposing cells
PT   to nucleic acid construct encoding hCG immunogenic epitope -
XX
PS   Example 1; Fig 2E; 45pp; English.
XX
CC   The present sequence comprises a fragment of the human her2 oncogene. It
CC   was used with fragments of the human chorionic gonadotrophin (hCG)
CC   beta-subunit cDNA to create a fusion molecule, which could then be used
CC   in the methods of the invention which involve the use of DNA vaccines
CC   encoding hCG antigens to induce an immune response and enable the
CC   treatment of cancer and provide a novel method of fertility control. In
CC   particular, they can be used to treat colorectal, breast and lung cancer,
CC   as hCG is associated with these types of tumours.
XX
SQ   Sequence 73 BP; 19 A; 24 C; 19 G; 11 T; 0 other;

  Query Match             1.8%;  Score 26;  DB 21;  Length 73;
  Best Local Similarity   62.1%;  Pred. No. 1.5e+03;
  Matches   41;  Conservative    0;  Mismatches   25;  Indels    0;  Gaps    0;

Qy     186 CTGGCCAAGACAGTGGCCTTCCTCAGGAACCTGCCATCCTTCTGGCAGCTGCCTCCCCAG 245
           | |  | ||||| |||     || | | |   | ||| || | |  |||  ||||||||||
Db       8 CCGTGCTAGACAATGGAGACCCGCTGAACAATACCACCCCTGTCACAGGGGCCTCCCCAG 67

Qy     246 GACCAG 251
           ||  ||
Db      68 GATAAG 73


RESULT 7
ABN40794/c
ID   ABN40794 standard; DNA; 60 BP.
XX
AC   ABN40794;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Human spliced transcript detection oligonucleotide SEQ ID NO:13542.
XX
KW   Human; mouse; rat; splice transcript; detection; RNA transcript;
KW   splice variant; transcriptome; oligonucleotide library; ss.
XX
OS   Homo sapiens.
XX
PN   WO200210449-A2.
XX
PD   07-FEB-2002.
XX
PF   20-JUL-2001; 2001WO-IB01903.
XX
PR   28-JUL-2000; 2000US-221607P.
PR   02-MAY-2001; 2001US-287724P.
XX
PA   (COMP-) COMPUGEN INC.
XX
PI   Shoshan A,  Wasserman A,  Mintz E,  Mintz L,  Faigler S;
XX
DR   WPI; 2002-257383/30.
XX
PT   New oligonucleotide libraries comprising oligonucleotides which
PT   selectively hybridize to mRNAs transcribed from a transcription unit of
PT   a genome, useful for detecting tissue-, pathology-, and
PT   developmental-specific genes -
XX
PS   Example 1; SEQ ID 13542; 47pp; English.
XX
CC   The present invention describes oligonucleotide libraries for detecting
CC   messenger RNAs that populate a (sub-)transcriptome, where the
CC   (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC   transcription units that populate a genome. The library comprises
CC   several oligonucleotides, each capable of hybridising selectively to a
CC   set of messenger RNAs transcribed from a given transcription unit of
CC   the genome, which encodes one or more messenger RNA splice variants.
CC   The oligonucleotide libraries are useful for detecting mRNAs from a
CC   biological sample, in expression profiling studies, in qualitatively or
CC   quantitatively characterising the corresponding transcriptome, and in
CC   detecting RNA transcripts and splice variants of human or animal
CC   transcriptomes. The libraries may also be used as specialised mini
CC   libraries to detect transcripts of a sub-transcriptome under a
CC   particular biological or pathological state, and so allowing the
CC   detection of tissue- and pathology-specific genes such as those genes
```

CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 60 BP; 16 A; 15 C; 11 G; 18 T; 0 other;

Query Match 1.8%; Score 25.8; DB 24; Length 60;
Best Local Similarity 73.3%; Pred. No. 1.5e+03;
Matches 33; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 562 ACTTGCCCAAGGTCACCCAGCTAATAAGTGACAGTGCTGGGATTC 606
||| || | || ||| ||| | |||||||||| |||| || ||
Db 60 ACTGGCTCTAGATCATGTAGCAATTAAGTGACAGAGCTGTGAATC 16

LT 8
AAH38784
ID AAH38784 standard; DNA; 47 BP.
XX
AC AAH38784;
XX
DT 14-AUG-2001 (first entry)
XX
DE Human SNP flanking oligonucleotide SEQ ID 1580.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; ds.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US28436.
XX
PR 15-OCT-1999; 99US-0160096.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI; 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample -
XX
PS Claim 1; Page 58; 83pp; English.
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a fragment of human
CC DNA flanking the site of a single nucleotide polymorphism.
XX
SQ Sequence 47 BP; 12 A; 15 C; 11 G; 9 T; 0 other;

Query Match 1.7%; Score 25.4; DB 22; Length 47;
Best Local Similarity 74.4%; Pred. No. 1.8e+03;
Matches 32; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 550 AGAGATTAAGTGACTTGCCCAAGGTCACCCAGCTAATAAGTGA 592
|||| | || |||||||||||| ||| ||||| || |||
Db 4 AGAGGTCCAGCCACTTGCCCAAGGCCACACAGCTCTTATTTGA 46

RESULT 9
ABN39098/c
ID ABN39098 standard; DNA; 60 BP.
XX
AC ABN39098;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:11846.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes -
XX
PS Example 1; SEQ ID 11846; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the

```
CC   detection of tissue- and pathology-specific genes such as those genes
CC   only expressed in specific tissue under a specific pathological
CC   condition; to detect developmental specific genes; and to detect RNA
CC   transcripts and splice variants of a transcriptome of a patient suffering
CC   from a particular disorder. ABN27253 to ABN59589 represent
CC   oligonucleotide sequences from rats, humans and mice, which are used in
CC   the exemplification of the present invention.
CC   N.B. The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 60 BP; 14 A; 16 C; 15 G; 15 T; 0 other;

  Query Match             1.7%;  Score 25.4;  DB 24;  Length 60;
  Best Local Similarity   74.4%;  Pred. No. 2e+03;
  Matches   32;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy     562 ACTTGCCCAAGGTCACCCAGCTAATAAGTGACAGTGCTGGGAT 604
           |||| || |||||||| ||| |||||||||  ||||| ||
Db      56 ACTTTGCTGAGGTCACCTTGCTGCTAAGTGACACAGCTGGCAT 14


RESULT 10
AAT97276/c
ID   AAT97276 standard; DNA; 72 BP.
XX
AC   AAT97276;
XX
DT   11-MAR-1998  (first entry)
XX
DE   Nucleotide EP-13 SEQ ID NO:51 from J09278794 Example 7.
XX
KW   Hepatitis C virus; HCV; chimeric; antigen; detection; core region;
KW   epitope; NS3; NS4; infection; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   JP09278794-A.
XX
PD   28-OCT-1997.
XX
PF   10-FEB-1997;   97JP-0027015.
XX
PR   09-FEB-1996;   96JP-0024045.
XX
PA   (TOFU ) TONEN CORP.
XX
     WPI; 1998-022248/03.

     New chimeric peptide antigen derived from hepatitis C virus protein
PT   - useful for detecting HCV infections
XX
PS   Example 7; Page 14; 30pp; Japanese.
XX
CC   The present sequence represents a nucleotide sequence from example 7
CC   of the present invention describing a HCV chimeric peptide antigen
CC   which comprises at least 2 peptide epitope regions from the HCV
CC   polypeptide core region, 2 peptide epitope regions from the NS3 region
CC   and at least 2 peptide epitope regions from the NS4 region. The antigen
CC   binds specifically with an antibody produced by a human infected by
CC   HCV. The peptide can detect a wide range of HCV infections with high
CC   sensitivity.
XX
SQ   Sequence 72 BP; 15 A; 25 C; 21 G; 11 T; 0 other;

  Query Match             1.7%;  Score 25.4;  DB 19;  Length 72;
  Best Local Similarity   68.6%;  Pred. No. 2.2e+03;
  Matches   35;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy    1081 TGCTCAGGTGACCTGTTCCAGCCCAGGCAGAGATCAGGTGGGCAGAGGCTG 1131
           ||||| |||||||| ||||| |   || | | | | || || | | || ||
Db      70 TGCTCCGGTGACCTATTCCACCTACGGTAAATACCTGGCGGACGGCGGTTG 20


RESULT 11
ABN28389/c
ID   ABN28389 standard; DNA; 65 BP.
XX
AC   ABN28389;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Rat spliced transcript detection oligonucleotide SEQ ID NO:1137.
XX
KW   Human; mouse; rat; splice transcript; detection; RNA transcript;
KW   splice variant; transcriptome; oligonucleotide library; ss.
XX
OS   Rattus norvegicus.
XX
PN   WO200210449-A2.
XX
PD   07-FEB-2002.
XX
PF   20-JUL-2001; 2001WO-IB01903.
XX
PR   28-JUL-2000; 2000US-221607P.
PR   02-MAY-2001; 2001US-287724P.
XX
PA   (COMP-) COMPUGEN INC.
XX
PI   Shoshan A,  Wasserman A,  Mintz E,  Mintz L,  Faigler S;
XX
DR   WPI; 2002-257383/30.
XX
PT   New oligonucleotide libraries comprising oligonucleotides which
PT   selectively hybridize to mRNAs transcribed from a transcription unit of
PT   a genome, useful for detecting tissue-, pathology-, and
PT   developmental-specific genes
XX
PS   Example 1; SEQ ID 1137; 47pp; English.
XX
CC   The present invention describes oligonucleotide libraries for detecting
CC   messenger RNAs that populate a (sub-)transcriptome, where the
CC   (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC   transcription units that populate a genome. The library comprises
CC   several oligonucleotides, each capable of hybridising selectively to a
CC   set of messenger RNAs transcribed from a given transcription unit of
CC   the genome, which encodes one or more messenger RNA splice variants.
CC   The oligonucleotide libraries are useful for detecting mRNAs from a
CC   biological sample, in expression profiling studies, in qualitatively or
CC   quantitatively characterising the corresponding transcriptome, and in
CC   detecting RNA transcripts and splice variants of human or animal
CC   transcriptomes. The libraries may also be used as specialised mini
CC   libraries to detect transcripts of a sub-transcriptome under a
CC   particular biological or pathological state, and so allowing the
CC   detection of tissue- and pathology-specific genes such as those genes
CC   only expressed in specific tissue under a specific pathological
CC   condition; to detect developmental specific genes; and to detect RNA
CC   transcripts and splice variants of a transcriptome of a patient suffering
CC   from a particular disorder. ABN27253 to ABN59589 represent
CC   oligonucleotide sequences from rats, humans and mice, which are used in
CC   the exemplification of the present invention.
CC   N.B. The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 65 BP; 8 A; 23 C; 14 G; 20 T; 0 other;

  Query Match             1.7%;  Score 25.2;  DB 24;  Length 65;
  Best Local Similarity   71.7%;  Pred. No. 2.4e+03;
  Matches   33;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy     707 AGGAGGAGGTAGTAGTGGGACCTCAAAGGCCGAGCAAAGGAGGCAG 752
           |||| |||||  |||| || |   |||| || |  |  |||||||||
Db      63 AGGATGAGGTGGTAGGGGCATAGCAAAAGCTGCTCCCAGGAGGCAG 18
```

RESULT 12
AAL30738/c
ID AAL30738 standard; DNA; 51 BP.
XX
AC AAL30738;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #3946.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX
PS Claim 1; Page 2520; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.
XX
SQ Sequence 51 BP; 13 A; 5 C; 1 G; 32 T; 0 other;

Query Match 1.7%; Score 25; DB 22; Length 51;
Best Local Similarity 69.4%; Pred. No. 2.4e+03;
Matches 34; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1408 ATTAAGTTATTGATTTTTGTAATAAAAGGTATGAAACACTAAAAAAAAA 1456
Db 49 AGTAAAGTGCTTATTTTTGTAGTAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 13
AAZ67790
ID AAZ67790 standard; DNA; 47 BP.
XX
AC AAZ67790;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human map-related biallelic marker SEQ ID NO:2137.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(24,G)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB00822.
XX
PR 21-APR-1998; 98US-0082614.
PR 23-NOV-1998; 98US-0109732.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome -
XX
PS Claim 1; Page 686; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 47 BP; 16 A; 10 C; 11 G; 10 T; 0 other;

Query Match 1.7%; Score 24.8; DB 21; Length 47;
Best Local Similarity 72.7%; Pred. No. 2.6e+03;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 550 AGAGATTAAGTGACTTGCCCAAGGTCACCCAGCTAATAAGTGAC 593
Db 3 AGAAACAAGGAGACTTGCCCAAGGTCGTGCATCAATTAAGTGCC 46

RESULT 14
ABN47816
ID ABN47816 standard; DNA; 60 BP.
XX
AC ABN47816;

XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:20564.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes
XX
PS Example 1; SEQ ID 20564; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 60 BP; 20 A; 13 C; 15 G; 12 T; 0 other;

Query Match 1.7%; Score 24.6; DB 24; Length 60;
Best Local Similarity 65.5%; Pred. No. 3.5e+03;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 547 CCCAGAGATTAAGTGACTTGCCCAAGGTCACCCAGCTAATAAGTGACAGTGCTGG 601
|| |||| |||||| || ||| |||| || ||||| || | | | | ||
Db 1 CCTAGAGGTTAAGTTACCTGCTCAAGACAACGTAGCTAGTAGGAGCAAAGCCAGG 55

RESULT 15
AAL30269/c
ID AAL30269 standard; DNA; 51 BP.
XX
AC AAL30269;

XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #3477.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections
XX
PS Claim 1; Page 2383; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.
XX
SQ Sequence 51 BP; 12 A; 1 C; 2 G; 36 T; 0 other;

Query Match 1.7%; Score 24.4; DB 22; Length 51;
Best Local Similarity 68.0%; Pred. No. 3.6e+03;
Matches 34; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 1407 AATTAAGTTATTGATTTTTGTAATAAAAGGTATGAAACACTAAAAAAAAA 1456
||| || | || ||| || || ||||| . | ||| | |||||||||
Db 51 AATAAAAATCTTTATTCTTTTAGTAAAAAAAAAAAAAAAAAAAAAAAAA 2

Search completed: October 31, 2002, 21:55:33
Job time : 253 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: October 31, 2002, 19:54:31 ; Search time 2921 Seconds
(without alignments)
14506.568 Million cell updates/sec

Title: US-09-919-197-3
Perfect score: 1456
Sequence: 1 tgagcaccagccaaccaggg.....tatgaaacactaaaaaaaaa 1456

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

1 number of hits satisfying chosen parameters: 941340

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	31.4	2.2	49	6	A65431	A65431 Sequence 23
c	2	29.4	2.0	71	4	AF055530	AF055530 Didelphis
	3	25.4	1.7	47	6	AX116457	AX116457 Sequence
c	4	25.4	1.7	72	6	E14197	E14197 PCR primer
	5	24.6	1.7	64	9	HS001823	AJ001823 Homo sapi
	6	23.8	1.6	64	6	E40916	E40916 Humanized a
	7	23.8	1.6	75	6	A05173	A05173 Oligonucleo
c	8	23.6	1.6	60	6	AR117953	AR117953 Sequence
c	9	23.6	1.6	71	6	AR020462	AR020462 Sequence
c	10	23.6	1.6	71	6	AR054774	AR054774 Sequence
c	11	23.6	1.6	71	6	AR066039	AR066039 Sequence
c	12	23.4	1.6	75	6	A15067	A15067 Nucleotide
	13	23	1.6	74	6	A08223	A08223 synthetic o
c	14	23	1.6	74	6	A08224	A08224 synthetic o
c	15	22.8	1.6	74	8	CBE345111	AJ345111 Carpinus
	16	22.6	1.6	50	6	AX199582	AX199582 Sequence
	17	22.6	1.6	65	6	AX482787	AX482787 Sequence
	18	22.4	1.5	50	6	AX199690	AX199690 Sequence
c	19	22.4	1.5	54	6	AR139994	AR139994 Sequence
c	20	22.4	1.5	65	6	AX485185	AX485185 Sequence
	21	22.2	1.5	48	6	AR184251	AR184251 Sequence
	22	22.2	1.5	48	6	AR184372	AR184372 Sequence
	23	22.2	1.5	48	6	AX127963	AX127963 Sequence
c	24	22.2	1.5	55	6	AX002002	AX002002 Sequence
	25	22.2	1.5	55	6	E40050	E40050 Drug contai
	26	22.2	1.5	55	6	E40858	E40858 Humanized a
	27	22.2	1.5	55	6	E43404	E43404 Humanized a
c	28	22.2	1.5	61	6	AR051730	AR051730 Sequence
c	29	22.2	1.5	61	6	AR117040	AR117040 Sequence
c	30	22.2	1.5	61	6	AR200053	AR200053 Sequence
c	31	22.2	1.5	61	6	I20500	I20500 Sequence 22
c	32	22.2	1.5	61	6	I49676	I49676 Sequence 20
c	33	22.2	1.5	63	6	BD002020	BD002020 Construct
c	34	22.2	1.5	63	6	I08751	I08751 Sequence 13
	35	22.2	1.5	65	6	AR117041	AR117041 Sequence
	36	22.2	1.5	65	6	AR200054	AR200054 Sequence
	37	22.2	1.5	65	6	I20501	I20501 Sequence 23
	38	22.2	1.5	65	6	I49677	I49677 Sequence 21
c	39	22.2	1.5	69	6	I16689	I16689 Sequence 29
c	40	22.2	1.5	69	6	I89442	I89442 Sequence 29
c	41	22.2	1.5	70	6	AX328443	AX328443 Sequence
	42	22	1.5	39	6	AX137540	AX137540 Sequence
	43	22	1.5	51	6	AX162353	AX162353 Sequence
c	44	22	1.5	58	6	E03095	E03095 RNA encodin
c	45	22	1.5	59	9	S76156	S76156 delta-beta

ALIGNMENTS

RESULT 1
A65431/c
LOCUS A65431 49 bp DNA linear PAT 29-MAR-1999
DEFINITION Sequence 23 from Patent WO9735005.
ACCESSION A65431
VERSION A65431.1 GI:4531190
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 49)
AUTHORS Harris,A.
TITLE CFTR GENE REGULATOR
JOURNAL Patent: WO 9735005-A 23 25-SEP-1997;
ISIS INNOVATION (GB)

```
COMMENT     Other publication AU 2036897 19971010.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT       15 a     10 c      5 g     19 t
ORIGIN

  Query Match             2.2%;  Score 31.4;  DB 6;  Length 49;
  Best Local Similarity   77.6%;  Pred. No. 1.8e+03;
  Matches   38;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy     557 AAGTGACTTGCCCAAGGTCACCCAGCTAATAAGTGACAGTGCTGGGATT 605
           |||| | ||||| ||| ||||   | ||||||||||||| | | |||||
Db      49 AAGTAAATTGCCTAAGATCACATTGTTAATAAGTGACAGAGTTAGGATT 1


RESULT 2
AF055530/c
     S        AF055530                 71 bp    DNA     linear   MAM 16-OCT-2001
     NITION   Didelphis virginiana isolate O51 retroposon CORE-SINE Mar-1
              sequence.
ACCESSION     AF055530
VERSION       AF055530.1  GI:4511910
KEYWORDS      .
SOURCE        Didelphis virginiana.
  ORGANISM    Didelphis virginiana
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
REFERENCE     1  (bases 1 to 71)
  AUTHORS     Gilbert,N. and Labuda,D.
  TITLE       Evolutionary inventions and continuity of CORE-SINEs in mammals
  JOURNAL     J. Mol. Biol. 298 (3), 365-377 (2000)
  MEDLINE     20237720
   PUBMED     10772856
FEATURES             Location/Qualifiers
     source          1. .71
                     /organism="Didelphis virginiana"
                     /isolate="O51"
                     /db_xref="taxon:9267"
     repeat_region   1. .71
                     /rpt_family="retroposon CORE-SINE Mar-1"
                     /rpt_type=dispersed
BASE COUNT       14 a     19 c     15 g     23 t
ORIGIN

  Query Match             2.0%;  Score 29.4;  DB 4;  Length 71;
  Best Local Similarity   79.7%;  Pred. No. 6.9e+03;
  Matches   47;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy     529 CCGATAAAGAAACTGAAGCCCAGA-GATTAAGTGACTTGCCCAAGGTCACCCAGCTAAT 586
           | ||| | |||||||| ||| | | | | || ||||||||||||||||||| |||||| |
Db      63 CAGATGAGGAAACTGAGGCCAACAGGGTGAAATGACTTGCCCAAGGTCACACAGCTAGT 5


RESULT 3
AX116457
LOCUS         AX116457                 47 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION    Sequence 1580 from Patent WO0129262.
ACCESSION     AX116457
VERSION       AX116457.1  GI:14033399
KEYWORDS      .
SOURCE        human.
  ORGANISM    Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1  (bases 1 to 47)
  AUTHORS     Picoult-Newburg,L. and Pohl,M.
  TITLE       Genotyping reagents, kits and methods of use thereof
  JOURNAL     Patent: WO 0129262-A 1580 26-APR-2001;
              Orchid BioSciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT       12 a     15 c     11 g      9 t
ORIGIN

  Query Match             1.7%;  Score 25.4;  DB 6;  Length 47;
  Best Local Similarity   74.4%;  Pred. No. 8.1e+04;
  Matches   32;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy     550 AGAGATTAAGTGACTTGCCCAAGGTCACCCAGCTAATAAGTGA 592
           |||| |  ||  |||||||||||| ||| |||||  ||  |||
Db       4 AGAGGTCCAGCCACTTGCCCAAGGCCACACAGCTCTTATTTGA 46


RESULT 4
E14197/c
LOCUS         E14197                   72 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION    PCR primer for gaining C7 region epitope of HCV.
ACCESSION     E14197
VERSION       E14197.1  GI:5708880
KEYWORDS      JP 1997278794-A/40.
SOURCE        unidentified.
  ORGANISM    unidentified
              unclassified.
REFERENCE     1  (bases 1 to 72)
  AUTHORS     Yamaguchi,K., Kashiwaguma,T., Chiba,Y., Yagi,S. and Hasegawa,A.
  TITLE       CHIMERA ANTIGEN PEPTIDE
  JOURNAL     Patent: JP 1997278794-A 40 28-OCT-1997;
              TONEN CORP.
COMMENT       OS   None
              OC   Artificial sequences.
              PN   JP 1997278794-A/40
              PD   28-OCT-1997
              PF   10-FEB-1997 JP 1997027015
              PR   09-FEB-1996 JP 96P    24045
              PI   YAMAGUCHI KENJIRO, KASHIWAGUMA TOMIKO, CHIBA YUKIE, PI   YAGI
              SHINTARO,
              PI   HASEGAWA AKIRA
              PC   C07K14/18,C07H21/04,C07K19/00,C12N15/09,C12P21/02,G01N33/53,
              PC   G01N33/576//
              PC   C12N1/21,(C12P21/02,C12R1:19),(C12N1/21,C12R1:19); CC
              strandedness: Single;
              CC   topology: Linear;
              CC   hypothetical: No;
              CC   anti-sense: Yes;
              FH   Key             Location/Qualifiers
              FH
              FT   source          1. .72
              FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .72
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT       15 a     25 c     21 g     11 t
ORIGIN

  Query Match             1.7%;  Score 25.4;  DB 6;  Length 72;
  Best Local Similarity   68.6%;  Pred. No. 8.7e+04;
  Matches   35;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy    1081 TGCTCAGGTGACCTGTTCCAGCCCAGGCAGAGATCAGGTGGGCAGAGGCTG 1131
           ||||| |||||||| ||||| |  || | | | | || || | | || ||
Db      70 TGCTCCGGTGACCTATTCCACCTACGGTAAATACCTGGCGGACGGCGGTTG 20


RESULT 5
HS001823
LOCUS         HS001823                 64 bp    DNA     linear   PRI 30-SEP-1997
DEFINITION    Homo sapiens exon 2E4 from Los Alamos contig C159.1, chromosome
              16p12.2.
ACCESSION     AJ001823
VERSION       AJ001823.1  GI:2462356
KEYWORDS      .
```

```
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 64)
  AUTHORS   Greenham,J.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-SEP-1997) Greenham J.A., Paediatrics, University
            College London Medical School, The Rayne Institute, 5 University
            Street, London., WC1E 6JJ, U.K
REFERENCE   2  (bases 1 to 64)
  AUTHORS   Greenham,J.A.
  TITLE     The identification and integration of transcripts mapping to human
            chromosome 16p12.2 - p12.1
  JOURNAL   Unpublished
FEATURES             Location/Qualifiers
     source          1. .64
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="16"
                     /map="p12.2"
     exon            1. .64
                     /note="2E4"
BASE COUNT       20 a     13 c     16 g     14 t      1 others
ORIGIN

  Query Match             1.7%;  Score 24.6;  DB 9;  Length 64;
  Best Local Similarity   76.9%;  Pred. No. 1.4e+05;
  Matches   30;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy     554 ATTAAGTGACTTGCCCAAGGTCACCCAGCTAATAAGTGA 592
           ||||  ||| |  |||| |||||| ||||||||  ||||
Db      25 ATTACATGATTACCCCAGGGTCACACAGCTAATTGGTGA 63


RESULT 6
E40916
LOCUS       E40916                    64 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Humanized anti-Fas antibody.
ACCESSION   E40916
VERSION     E40916.1  GI:18627493
KEYWORDS    JP 2000166574-A/105.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 64)
  AUTHORS   Serizawa,N., Haruyama,H., Nakahara,K. and Tamaki,I.
  TITLE     Humanized anti-Fas antibody
  JOURNAL   Patent: JP 2000166574-A 105 20-JUN-2000;
            SANKYO CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000166574-A/105
            PD   20-JUN-2000
            PF   29-SEP-1999 JP 1999275441
            PR
            PI   NOBUKI SERIZAWA,HIDEYUKI HARUYAMA,KAORI NAKAHARA,IKUKO TAMAKI
            PC   C12N15/09,A61K39/00,A61K39/395,A61K39/395,A61P37/02,A61P43/00,
            PC   C07K16/18,
            PC   C12N1/21,C12N5/10,C12P21/08//(C12N1/21,C12R1:19),C12N15/00, PC
              C12N5/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .64
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .64
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT       14 a     16 c     23 g     11 t
ORIGIN

  Query Match             1.6%;  Score 23.8;  DB 6;  Length 64;
  Best Local Similarity   72.1%;  Pred. No. 2.3e+05;
  Matches   31;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy     309 GCTGTGACCTTTGAGGTGGCTGAGGCCCCGGTGCCCAGCATAC 351
           | || | |||| | || ||||||||   ||||| |||| |||
Db       7 GATGGGCCCTTGGTGGAGGCTGAGGAGACGGTGACCAGTGTAC 49


RESULT 7
A05173
LOCUS       A05173                    75 bp    DNA     linear   PAT 30-APR-1993
DEFINITION  Oligonucleotide probe corresponding to the CS protein of Corpuscles
            of Stannius.
ACCESSION   A05173
VERSION     A05173.1  GI:345032
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
FEATURES             Location/Qualifiers
     source          1. .75
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT       15 a     21 c     28 g     11 t
ORIGIN

  Query Match             1.6%;  Score 23.8;  DB 6;  Length 75;
  Best Local Similarity   72.1%;  Pred. No. 2.4e+05;
  Matches   31;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy     156 CATCGCACCTGCCGGGAGGCCTTGGATGTTCTGGCCAAGACAG 198
           |||| ||||||| |||   | ||   |||||||||||| | | |
Db      14 CATCCCACCTGCAGGGCTCCGTTCAGTGTTCTGGCCACGTCGG 56


RESULT 8
AR117953/c
LOCUS       AR117953                  60 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 45 from patent US 6140470.
ACCESSION   AR117953
VERSION     AR117953.1  GI:14098859
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 60)
  AUTHORS   Garen,A. and Cai,X.
  TITLE     Human monoclonal anti-tumor antibodies
  JOURNAL   Patent: US 6140470-A 45 31-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .60
                     /organism="unknown"
BASE COUNT        7 a     26 c     15 g      7 t      5 others
ORIGIN

  Query Match             1.6%;  Score 23.6;  DB 6;  Length 60;
  Best Local Similarity   66.7%;  Pred. No. 2.6e+05;
  Matches   32;  Conservative    1;  Mismatches   15;  Indels    0;  Gaps    0;

Qy     694 TTACCTCCTCTAAAGGAGGAGGTAGTAGTGGGACCTCAAAGGCCGAGC 741
           |.|||  |||:  |||||| ||  |||| ||| || |   |||||| |
Db      50 TCACCGTCTCYTCAGGAGGCGGGGGTAGCGGGGCCGCTGGGGCCGAAC 3


RESULT 9
AR020462/c
LOCUS       AR020462                  71 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 2 from patent US 5789163.
ACCESSION   AR020462
VERSION     AR020462.1  GI:3975077
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
```

```
REFERENCE   1  (bases 1 to 71)
  AUTHORS   Drolet,D.W., Jayasena,S.D. and Gold,L.
  TITLE     Enzyme linked oligonucleotide assays (ELONAS)
  JOURNAL   Patent: US 5789163-A 2 04-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .71
                     /organism="unknown"
BASE COUNT       15 a     16 c     33 g      7 t
ORIGIN

  Query Match             1.6%;  Score 23.6;  DB 6;  Length 71;
  Best Local Similarity   69.6%;  Pred. No. 2.7e+05;
  Matches   32;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy    952 GCCGCCTGACCCGTGTCCTCCTCACGGCCTCCACCCTCAAGTCCAT 997
          | || ||| || ||  ||||| |  | |||||||| |||| | || |
Db     63 GTCGTCTGGCCAGTCCCCTCCACGTGCCCTCCACACTCAGGCCCTT 18


RESULT 10
AR054774/c
LOCUS       AR054774                 71 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 5 from patent US 5837456.
ACCESSION   AR054774
VERSION     AR054774.1  GI:5980351
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 71)
  AUTHORS   Gold,L., Jayasena,S.D., Nieuwlandt,D. and Davis,K.
  TITLE     High affinity oligonucleotide ligands to chorionic gonadotropin
            hormone and related glycoprotein hormones
  JOURNAL   Patent: US 5837456-A 5 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .71
                     /organism="unknown"
BASE COUNT       15 a     16 c     33 g      7 t
ORIGIN

  Query Match             1.6%;  Score 23.6;  DB 6;  Length 71;
  Best Local Similarity   69.6%;  Pred. No. 2.7e+05;
  Matches   32;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy    952 GCCGCCTGACCCGTGTCCTCCTCACGGCCTCCACCCTCAAGTCCAT 997
          | || ||| || ||  ||||| |  | |||||||| |||| | || |
Db     63 GTCGTCTGGCCAGTCCCCTCCACGTGCCCTCCACACTCAGGCCCTT 18


RESULT 11
AR066039/c
LOCUS       AR066039                 71 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 5 from patent US 5849890.
ACCESSION   AR066039
VERSION     AR066039.1  GI:5996255
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 71)
  AUTHORS   Gold,L., Jayasena,S.D., Nieuwlandt,D. and Davis,K.
  TITLE     High affinity oligonucleotide ligands to chorionic gonadotropin
            hormone and related glycoprotein hormones
  JOURNAL   Patent: US 5849890-A 5 15-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .71
                     /organism="unknown"
BASE COUNT       15 a     16 c     33 g      7 t
ORIGIN

  Query Match             1.6%;  Score 23.6;  DB 6;  Length 71;
  Best Local Similarity   69.6%;  Pred. No. 2.7e+05;
  Matches   32;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy    952 GCCGCCTGACCCGTGTCCTCCTCACGGCCTCCACCCTCAAGTCCAT 997
          | || ||| || ||  ||||| |  | |||||||| |||| | || |
Db     63 GTCGTCTGGCCAGTCCCCTCCACGTGCCCTCCACACTCAGGCCCTT 18


RESULT 12
A15067/c
LOCUS       A15067                   75 bp    DNA     linear   PAT 07-FEB-1994
DEFINITION  Nucleotide sequence 8 from patent number EP0206863.
ACCESSION   A15067
VERSION     A15067.1  GI:492830
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 75)
  AUTHORS   Roskam,W. and Ferrara,P.
  TITLE     Non-amidated derivatives of somatocrinine and process for the
            preparation by genetic engineering
  JOURNAL   Patent: EP 0206863-A 8 30-DEC-1986;
            SANOFI S.A
FEATURES             Location/Qualifiers
     source          1. .75
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT       17 a     21 c     24 g     13 t
ORIGIN

  Query Match             1.6%;  Score 23.4;  DB 6;  Length 75;
  Best Local Similarity   67.3%;  Pred. No. 3.1e+05;
  Matches   33;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy    255 CGGCTGCTGCAGGGTTGCTGGGGCCCCCTCTTCCTGCTTGGGTTGGCCC 303
          ||| | || ||||  |||  |||| ||    |||| || | || ||||
Db     75 CGGATCCTACAGGCGTGCACGGGCGCCACGCTCCTGGTTAGATTCGCCC 27


RESULT 13
A08223
LOCUS       A08223                   74 bp    DNA     linear   PAT 19-JUL-1993
DEFINITION  synthetic oligonucleotide primer Va.
ACCESSION   A08223
VERSION     A08223.1  GI:413428
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 74)
  AUTHORS   Seemann,G., Bosslet,K. and Sedlacek,H.H.
  TITLE     Antigens composed of major histocompatibility complex class I
            antigens and specific carrier molecules, their production and use
  JOURNAL   Patent: EP 0352761-A 5 31-JAN-1990;
            BEHRINGWERKE Aktiengesellschaft
FEATURES             Location/Qualifiers
     source          1. .74
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT       15 a     27 c     25 g      7 t
ORIGIN

  Query Match             1.6%;  Score 23;  DB 6;  Length 74;
  Best Local Similarity   68.1%;  Pred. No. 4e+05;
  Matches   32;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy    229 GGCAGCTGCCTCCCCAGGACCAGCGGCGGCTGCTGCAGGGTTGCTGG 275
          ||||||| || |  | | ||| || || || || ||||   || ||
Db     15 GGCAGCTCCCGCAGCTGCACCCGCAGCAGCCGCAGCAGGCGGGCAGG 61


RESULT 14
A08224/c
LOCUS       A08224                   74 bp    DNA     linear   PAT 19-JUL-1993
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DEFINITION  synthetic oligonucleotide primer Vb.
ACCESSION   A08224
VERSION     A08224.1  GI:413429
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 74)
  AUTHORS   Seemann,G., Bosslet,K. and Sedlacek,H.H.
  TITLE     Antigens composed of major histocompatibility complex class I
            antigens and specific carrier molecules, their production and use
  JOURNAL   Patent: EP 0352761-A 6 31-JAN-1990;
            BEHRINGWERKE Aktiengesellschaft
FEATURES             Location/Qualifiers
     source          1. .74
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        7 a     25 c     27 g     15 t
ORIGIN

  Query Match             1.6%;  Score 23;  DB 6;  Length 74;
  Best Local Similarity   68.1%;  Pred. No. 4e+05;
  Matches   32;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy    229 GGCAGCTGCCTCCCCAGGACCAGCGGCGGCTGCTGCAGGGTTGCTGG 275
          ||||||| || |  | | ||| || || || || |||||   || ||
Db     60 GGCAGCTCCCGCAGCTGCACCCGCAGCAGCCGCAGCAGGCGGGCAGG 14


RESULT 15
CBE345111/c
LOCUS       CBE345111                74 bp    DNA     circular PLN 04-JAN-2002
DEFINITION  Carpinus betulus chloroplast microsatellite, ccmp10 (3).
ACCESSION   AJ345111
VERSION     AJ345111.1  GI:18072971
KEYWORDS    satellite.
SOURCE      European hornbeam.
  ORGANISM  Carpinus betulus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fagales; Betulaceae; Carpinus.
REFERENCE   1
  AUTHORS   Grivet,D. and Petit,R.J.
  TITLE     Chloroplast DNA phylogeography of the hornbeam in Europe: evidence
            for a bottleneck at the outset of postglacial colonization
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 74)
  AUTHORS   Grivet,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-SEP-2001) Grivet D., Recherches forestieres, Inra,
            BP45, Gazinet Cedex, 33611, FRANCE
FEATURES             Location/Qualifiers
     source          1. .74
                     /organism="Carpinus betulus"
                     /db_xref="taxon:12990"
     repeat_unit     17. .32
                     /note="ccmp10 (3)"
BASE COUNT       19 a     11 c      6 g     38 t
ORIGIN

  Query Match             1.6%;  Score 22.8;  DB 8;  Length 74;
  Best Local Similarity   62.1%;  Pred. No. 4.5e+05;
  Matches   36;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy   1396 ATACAGAACTGAATTAAGTTATTGATTTTTGTAATAAAAGGTATGAAACACTAAAAAA 1453
          ||| | ||  |||||   || ||  | |||  || |||||  |  ||| |  |||| |
Db     72 ATAGAAAATCGAATTTGTTTCTTCGTCTTTACAAAAAAAGAAAAAAAAAAAAAAAATA 15


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GenCore version 5.1.3

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	25.4	1.7	72	4	US-09-020-846-51	Sequence 51, Appl
	2	23.6	1.6	60	3	US-08-983-607-45	Sequence 45, Appl
	3	23.6	1.6	71	1	US-08-487-425-2	Sequence 2, Appli
	4	23.6	1.6	71	2	US-08-488-402A-5	Sequence 5, Appli
c	5	23.6	1.6	71	2	US-08-484-552A-5	Sequence 5, Appli
c	6	23.6	1.6	71	2	US-08-628-356A-4	Sequence 4, Appli
c	7	23.6	1.6	71	5	PCT-US96-07439-2	Sequence 2, Appli
c	8	23.6	1.6	71	5	PCT-US96-09472-5	Sequence 5, Appli
c	9	22.4	1.5	54	4	US-09-257-581-1	Sequence 1, Appli
	10	22.2	1.5	48	4	US-09-425-638A-38	Sequence 38, Appl
	11	22.2	1.5	48	4	US-09-543-004-38	Sequence 38, Appl
c	12	22.2	1.5	61	1	US-07-609-716-22	Sequence 22, Appl
c	13	22.2	1.5	61	1	US-08-175-155-20	Sequence 20, Appl
c	14	22.2	1.5	61	1	US-08-477-509B-55	Sequence 55, Appl
c	15	22.2	1.5	61	2	US-08-707-237A-26	Sequence 26, Appl
c	16	22.2	1.5	61	3	US-08-482-085B-55	Sequence 55, Appl
c	17	22.2	1.5	61	3	US-08-475-411A-22	Sequence 22, Appl
c	18	22.2	1.5	61	4	US-08-478-029A-22	Sequence 22, Appl
c	19	22.2	1.5	61	4	US-09-444-791A-55	Sequence 55, Appl
	20	22.2	1.5	65	1	US-07-609-716-23	Sequence 23, Appl
	21	22.2	1.5	65	1	US-08-175-155-21	Sequence 21, Appl
	22	22.2	1.5	65	1	US-08-477-509B-56	Sequence 56, Appl
	23	22.2	1.5	65	3	US-08-482-085B-56	Sequence 56, Appl
	24	22.2	1.5	65	3	US-08-475-411A-23	Sequence 23, Appl
	25	22.2	1.5	65	4	US-08-478-029A-23	Sequence 23, Appl
	26	22.2	1.5	65	4	US-09-444-791A-56	Sequence 56, Appl
c	27	22.2	1.5	69	1	US-07-991-867B-29	Sequence 29, Appl
c	28	22.2	1.5	69	1	US-08-107-755A-29	Sequence 29, Appl
c	29	22.2	1.5	69	2	US-08-544-332-29	Sequence 29, Appl
c	30	22.2	1.5	69	4	US-09-370-861A-29	Sequence 29, Appl
c	31	22	1.5	58	6	5436330-3	Patent No. 5436330
c	32	22	1.5	61	1	US-08-055-390-4	Sequence 4, Appli
	33	22	1.5	75	4	US-09-042-353-173	Sequence 173, App
	34	22	1.5	75	4	US-08-758-417A-21	Sequence 21, Appl
c	35	21.8	1.5	47	4	US-09-641-638-928	Sequence 928, App
	36	21.8	1.5	71	2	US-08-488-402A-28	Sequence 28, Appl
	37	21.8	1.5	71	2	US-08-484-552A-28	Sequence 28, Appl
	38	21.8	1.5	71	5	PCT-US96-09472-28	Sequence 28, Appl
c	39	21.6	1.5	54	2	US-08-412-376-12	Sequence 12, Appl
c	40	21.6	1.5	54	2	US-08-412-376-26	Sequence 26, Appl
	41	21.6	1.5	63	5	PCT-US94-06079-39	Sequence 39, Appl
	42	21.6	1.5	70	4	US-09-042-353-172	Sequence 172, App
	43	21.6	1.5	70	4	US-08-758-417A-20	Sequence 20, Appl
	44	21.4	1.5	45	4	US-09-425-638A-13	Sequence 13, Appl
	45	21.4	1.5	45	4	US-09-543-004-13	Sequence 13, Appl

ALIGNMENTS

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RESULT 1
US-09-020-846-51/c
; Sequence 51, Application US/09020846
; Patent No. 6322965
;  GENERAL INFORMATION:
;    APPLICANT:  YAMAGUCHI, Kenjiro
;    APPLICANT:  KASHIWAKUMA, Tomiko
;    APPLICANT:  CHIBA, Yukie
;    APPLICANT:  YAGI, Shintaro
;    APPLICANT:  HASEGAWA, Akira
;    TITLE OF INVENTION:  CHIMERA ANTIGEN PEPTIDE
;    NUMBER OF SEQUENCES:  72
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY & LARDNER
;      STREET:  3000 K Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/020,846
;      FILING DATE:  09-FEB-1998
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 9-027015
;      FILING DATE:  10-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 8-024045
;      FILING DATE:  09-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wegner, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  053466/0225
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 672-5300
;      TELEFAX:  (202) 672-5399
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  72 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Synthetic DNA"
US-09-020-846-51
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  Query Match          1.7%;  Score 25.4;  DB 4;  Length 72;
  Best Local Similarity  68.6%;  Pred. No. 4.4e+02;
  Matches   35;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy   1081 TGCTCAGGTGACCTGTTCCAGCCCAGGCAGAGATCAGGTGGGCAGAGGCTG 1131
          ||||| |||||||| ||||| |   || | | | | || || | | || ||
Db     70 TGCTCCGGTGACCTATTCCACCTACGGTAAATACCTGGCGGACGGCGGTTG 20


RESULT 2
US-08-983-607-45/c
; Sequence 45, Application US/08983607
; Patent No. 6140470
;  GENERAL INFORMATION:
;    APPLICANT:  Alan Garen
;    APPLICANT:  Xiaohong Cai
;    TITLE OF INVENTION:  Human Anti-Tumor Monoclonal Anti-
;    TITLE OF INVENTION:  bodies
;    NUMBER OF SEQUENCES:  51
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Department of Molecular Biophysics
;      ADDRESSEE:  and Biochemistry, Yale University
;      STREET:  266 Whitney Avenue
;      CITY:  New Haven
;      STATE:  Connecticut
;      COUNTRY:  United States of America
;      ZIP:  06520-8114
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" 1.44 Mb diskette
;      COMPUTER:  IBM PC
;      OPERATING SYSTEM:  MS DOS
;      SOFTWARE:  Word Processing
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/983,607
;      FILING DATE:  April 27, 1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/IB96/01032
;      FILING DATE:  June 28, 1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mary M. Krinsky
;      REGISTRATION NUMBER:  32423
;      REFERENCE/DOCKET NUMBER:  OCR-679
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  203-773-9544
;      TELEFAX:  203-773-1183
;  INFORMATION FOR SEQ ID NO:  45:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  60 residues
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;      DESCRIPTION:  primer used in constructs
US-08-983-607-45

  Query Match          1.6%;  Score 23.6;  DB 3;  Length 60;
  Best Local Similarity  66.7%;  Pred. No. 1.3e+03;
  Matches   32;  Conservative    1;  Mismatches   15;  Indels    0;  Gaps    0;

Qy    694 TTACCTCCTCTAAAGGAGGAGGTAGTAGTGGGACCTCAAAGGCCGAGC 741
          | |||  |||: |||||| ||  |||| ||| || |   |||||| |
Db     50 TCACCGTCTCYTCAGGAGGCGGGGGTAGCGGGGCCGCTGGGGCCGAAC 3


RESULT 3
US-08-487-425-2/c
; Sequence 2, Application US/08487425
; Patent No. 5789163
;  GENERAL INFORMATION:
;    APPLICANT:  DROLET, DAN
;    APPLICANT:  JAYASENA, SUMEDHA
;    APPLICANT:  GOLD, LARRY
;    TITLE OF INVENTION:  ENZYME LINKED OLIGONUCLEOTIDE
;    TITLE OF INVENTION:  ASSAYS
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Swanson & Bratschun, L.L.C.
;      STREET:  8400 E. Prentice Avenue, Suite 200
;      CITY:  Englewood
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3 1/2 diskette, 1.44 MB
;      COMPUTER:  IBM pc compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,425
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/714,131
;      FILING DATE:  10-JUNE-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/536,428
;      FILING DATE:  11-JUNE-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/964,624
;      FILING DATE:  21-OCTOBER-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/234,997
;      FILING DATE:  28-APRIL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Barry J. Swanson
;      REGISTRATION NUMBER:  33,215
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 793-3333
;      TELEFAX:  (303) 793-3433
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  71 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  RNA
;    FEATURE:
;      OTHER INFORMATION:  All C's are 2'-NH2 cytosine
;    FEATURE:
;      OTHER INFORMATION:  All U's are 2'-NH2 uracil
US-08-487-425-2

  Query Match          1.6%;  Score 23.6;  DB 1;  Length 71;
  Best Local Similarity  69.6%;  Pred. No. 1.4e+03;
  Matches   32;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy    952 GCCGCCTGACCCGTGTCCTCCTCACGGCCTCCACCCTCAAGTCCAT 997
          | ||  ||| || ||  |||| |  | ||||||| |||| | || |
Db     63 GTCGTCTGGCCAGTCCCCTCCACGTGCCCTCCACACTCAGGCCCTT 18


RESULT 4
US-08-488-402A-5/c
; Sequence 5, Application US/08488402A
; Patent No. 5837456
;  GENERAL INFORMATION:
;    APPLICANT:  GOLD ET AL.
;    TITLE OF INVENTION:  HIGH AFFINITY OLIGONUCLEOTIDE LIGANDS TO
;    TITLE OF INVENTION:  CHORIONIC GONADOTROPIN HORMONE AND RELATED GLYCOPROTEIN
;    TITLE OF INVENTION:  HORMONES
;    NUMBER OF SEQUENCES:  160
;    CORRESPONDENCE ADDRESS:
```

```
;       ADDRESSEE:  Swanson & Bratschun, L.L.C.
;       STREET:  8400 E. Prentice Avenue, Suite 200
;       CITY:  Englewood
;       STATE:  Colorado
;       COUNTRY:  USA
;       ZIP:  80111
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette, 3 1/2 diskette, 1.44 MG
;       COMPUTER:  IBM pc compatible
;       OPERATING SYSTEM:  MS-DOS
;       SOFTWARE:  WordPerfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/488,402A
;       FILING DATE:  07 JUNE 1995
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/536,428
;       FILING DATE:  11-JUNE-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/714,131
;       FILING DATE:  10-JUNE-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/931,473
;       FILING DATE:  17-AUGUST-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/964,624
;       FILING DATE:  21-OCTOBER-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/177,991
;       FILING DATE:  8-SEPTEMBER-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Barry J. Swanson
;       REGISTRATION NUMBER:  33,215
;       REFERENCE/DOCKET NUMBER:  NEX36-1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (303) 793-3333
;       TELEFAX:  (303) 793-3433
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  71 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     FEATURE:
;       OTHER INFORMATION:  All C's are 2'-NH2 modified
;     FEATURE:
;       OTHER INFORMATION:  All U's are 2'-NH2 modified
US-08-488-402A-5

  Query Match             1.6%;  Score 23.6;  DB 2;  Length 71;
  Best Local Similarity   69.6%;  Pred. No. 1.4e+03;
  Matches   32;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy     952 GCCGCCTGACCCGTGTCCTCCTCACGGCCTCCACCCTCAAGTCCAT 997
           | || ||| || ||  ||||| |  | |||||||| |||| | || |
Db      63 GTCGTCTGGCCAGTCCCCTCCACGTGCCCTCCACACTCAGGCCCTT 18


RESULT 5
US-08-484-552A-5/c
; Sequence 5, Application US/08484552A
; Patent No. 5849890
;  GENERAL INFORMATION:
;    APPLICANT:  GOLD, LARRY
;    APPLICANT:  JAYASENA, SUMEDHA
;    APPLICANT:  NIEUWLANDT, DAN
;    APPLICANT:  DAVIS, KEN
;    TITLE OF INVENTION:  HIGH AFFINITY OLIGONUCLEOTIDE LIGANDS TO CHORIONIC
;    TITLE OF INVENTION:  GONADOTROPIN HORMONE AND RELATED GLYCOPROTEIN HORMONES
;    NUMBER OF SEQUENCES:  160
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Swanson & Bratschun, L.L.C.
;      STREET:  8400 E. Prentice Avenue, Suite 200
;      CITY:  Englewood
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3 1/2 diskette, 1.44 MG
;      COMPUTER:  IBM pc compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,552A
;      FILING DATE:  07 JUNE 1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/536,428
;      FILING DATE:  11-JUNE-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/714,131
;      FILING DATE:  10-JUNE-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/931,473
;      FILING DATE:  17-AUGUST-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/964,624
;      FILING DATE:  21-OCTOBER-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/177,991
;      FILING DATE:  8-SEPTEMBER-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Barry J. Swanson
;      REGISTRATION NUMBER:  33,215
;      REFERENCE/DOCKET NUMBER:  NEX36-2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 793-3333
;      TELEFAX:  (303) 793-3433
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  71 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      OTHER INFORMATION:  All C's are 2'-NH2 modified
;    FEATURE:
;      OTHER INFORMATION:  All U's are 2'-NH2 modified
US-08-484-552A-5

  Query Match             1.6%;  Score 23.6;  DB 2;  Length 71;
  Best Local Similarity   69.6%;  Pred. No. 1.4e+03;
  Matches   32;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy     952 GCCGCCTGACCCGTGTCCTCCTCACGGCCTCCACCCTCAAGTCCAT 997
           | || ||| || ||  ||||| |  | |||||||| |||| | || |
Db      63 GTCGTCTGGCCAGTCCCCTCCACGTGCCCTCCACACTCAGGCCCTT 18


RESULT 6
US-08-628-356A-4/c
; Sequence 4, Application US/08628356A
; Patent No. 5874218
;  GENERAL INFORMATION:
;    APPLICANT:  Drolet, Daniel W.
;    APPLICANT:  Jayasena, Sumedha
;    APPLICANT:  Gold, Larry
;    TITLE OF INVENTION:  Method for Detecting a Target
;    TITLE OF INVENTION:  Compound in a Substance Using a
;    TITLE OF INVENTION:  Nucleic Acid Ligand
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Swanson & Bratschun, L.L.C.
;      STREET:  8400 E. Prentice Place, Suite 200
;      CITY:  Englewood
;      STATE:  Colorado
```

```
;       ZIP:  80111
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5 inch disc
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  WordPerfect 6.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/628,356A
;       FILING DATE:  05-APRIL-1996
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/409,442
;       FILING DATE:  24-MARCH-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/714,131
;       FILING DATE:  10-JUNE-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/536,428
;       FILING DATE:  11-JUNE-1990
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Barry J. Swanson
;       REGISTRATION NUMBER:  33,215
;       REFERENCE/DOCKET NUMBER:  NEX54
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (303) 793-3333
;       TELEFAX:  (303) 793-3433
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  71 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     FEATURE:
;       OTHER INFORMATION:  All C's are 2'-amino
;       OTHER INFORMATION:  cytosine.
;     FEATURE:
;       OTHER INFORMATION:  All U's are 2'-amino
;       OTHER INFORMATION:  uridine.
US-08-628-356A-4

  Query Match             1.6%;  Score 23.6;  DB 2;  Length 71;
  Best Local Similarity   69.6%;  Pred. No. 1.4e+03;
  Matches   32;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy     952 GCCGCCTGACCCGTGTCCTCCTCACGGCCTCCACCCTCAAGTCCAT 997
           | || ||| || ||  ||||| |  | ||||||| |||| | || |
Db      63 GTCGTCTGGCCAGTCCCCTCCACGTGCCCTCCACACTCAGGCCCTT 18


RESULT 7
PCT-US96-07439-2/c
; Sequence 2, Application PC/TUS9607439
;  GENERAL INFORMATION:
;     APPLICANT:  DROLET, DAN
;     APPLICANT:  JAYASENA, SUMEDHA
;     APPLICANT:  GOLD, LARRY
;     TITLE OF INVENTION:  ENZYME LINKED OLIGONUCLEOTIDE
;     TITLE OF INVENTION:  ASSAYS
;     NUMBER OF SEQUENCES:  3
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Swanson & Bratschun, L.L.C.
;       STREET:  8400 E. Prentice Avenue, Suite 200
;       CITY:  Englewood
;       STATE:  Colorado
;       COUNTRY:  USA
;       ZIP:  80111
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette, 3 1/2 diskette, 1.44 MB
;       COMPUTER:  IBM pc compatible
;       OPERATING SYSTEM:  MS-DOS
;       SOFTWARE:  WordPerfect 6.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US96/07439
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/487,425
;       FILING DATE:  07-JUNE-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/714,131
;       FILING DATE:  10-JUNE-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/536,428
;       FILING DATE:  11-JUNE-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/964,624
;       FILING DATE:  21-OCTOBER-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/234,997
;       FILING DATE:  28-APRIL-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Barry J. Swanson
;       REGISTRATION NUMBER:  33,215
;       REFERENCE/DOCKET NUMBER:  NEX37/PCT
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (303) 793-3333
;       TELEFAX:  (303) 793-3433
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  71 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  RNA
;     FEATURE:
;       OTHER INFORMATION:  All C's are 2'-NH2 cytosine
;     FEATURE:
;       OTHER INFORMATION:  All U's are 2'-NH2 uracil
PCT-US96-07439-2

  Query Match             1.6%;  Score 23.6;  DB 5;  Length 71;
  Best Local Similarity   69.6%;  Pred. No. 1.4e+03;
  Matches   32;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy     952 GCCGCCTGACCCGTGTCCTCCTCACGGCCTCCACCCTCAAGTCCAT 997
           | || ||| || ||  ||||| |  | ||||||| |||| | || |
Db      63 GTCGTCTGGCCAGTCCCCTCCACGTGCCCTCCACACTCAGGCCCTT 18


RESULT 8
PCT-US96-09472-5/c
; Sequence 5, Application PC/TUS9609472
;  GENERAL INFORMATION:
;     APPLICANT:  GOLD ET AL.
;     TITLE OF INVENTION:  HIGH AFFINITY OLIGONUCLEOTIDE
;     TITLE OF INVENTION:  LIGANDS TO CHORIONIC GONADOTROPIN HORMONE AND RELATED
;     TITLE OF INVENTION:  GLYCOPROTEIN HORMONES
;     NUMBER OF SEQUENCES:  160
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Swanson & Bratschun, L.L.C.
;       STREET:  8400 E. Prentice Avenue, Suite 200
;       CITY:  Englewood
;       STATE:  Colorado
;       COUNTRY:  USA
;       ZIP:  80111
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette, 3 1/2 diskette, 1.44 MG
;       COMPUTER:  IBM pc compatible
;       OPERATING SYSTEM:  MS-DOS
;       SOFTWARE:  WordPerfect 6.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US96/09472
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:  08/488,402
;       APPLICATION NUMBER:
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;      FILING DATE:  07 JUNE 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/484,552
;      FILING DATE:  07 JUNE 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Barry J. Swanson
;      REGISTRATION NUMBER:  33,215
;      REFERENCE/DOCKET NUMBER:  NEX36-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 793-3333
;      TELEFAX:  (303) 793-3433
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  71 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      OTHER INFORMATION:  All C's are 2'-NH2 modified
;    FEATURE:
;      OTHER INFORMATION:  All U's are 2'-NH2 modified
;   US96-09472-5

  Query Match             1.6%;  Score 23.6;  DB 5;  Length 71;
  Best Local Similarity   69.6%;  Pred. No. 1.4e+03;
  Matches   32;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy    952 GCCGCCTGACCCGTGTCCTCCTCACGGCCTCCACCCTCAAGTCCAT 997
          | || ||| || ||  ||||| |  | ||||||| |||| | || |
Db     63 GTCGTCTGGCCAGTCCCCTCCACGTGCCCTCCACACTCAGGCCCTT 18


RESULT 9
US-09-257-581-1/c
; Sequence 1, Application US/09257581
; Patent No. 6207419
; GENERAL INFORMATION:
;  APPLICANT: Church, Frank C.
;  APPLICANT: Bauman, Susannah J.
;  TITLE OF INVENTION: THROMBIN INHIBITORY AGENTS AND METHODS OF USING SAME
;  FILE REFERENCE: 5470-232
;  CURRENT APPLICATION NUMBER: US/09/257,581
;  CURRENT FILING DATE: 1999-02-25
;  EARLIER APPLICATION NUMBER: 60/076,210
;  EARLIER FILING DATE: 1998-02-27
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;  LENGTH: 54
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence:primer
US-09-257-581-1

  Query Match             1.5%;  Score 22.4;  DB 4;  Length 54;
  Best Local Similarity   72.5%;  Pred. No. 2.6e+03;
  Matches   29;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy    690 TAAATTACCTCCTCTAAAGGAGGAGGTAGTAGTGGGACCT 729
          || |   || |||||  || || ||| || |||||||||
Db     52 TAGACCTCCACCTCTAGTGGTGGTGGTGGTGGTGGGACCT 13


RESULT 10
US-09-425-638A-38
; Sequence 38, Application US/09425638A
; Patent No. 6342587
; GENERAL INFORMATION:
;  APPLICANT:      Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
;  APPLICANT:  Lloyd J. Old
;  TITLE OF INVENTION:      A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO
;  FILE REFERENCE:      LUD 5630
;  CURRENT APPLICATION NUMBER: US/09/425,638A
;  CURRENT FILING DATE:  1999-10-22
;  NUMBER OF SEQ ID NOS:      129
; SEQ ID NO 38
;  LENGTH: 48
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
US-09-425-638A-38

  Query Match             1.5%;  Score 22.2;  DB 4;  Length 48;
  Best Local Similarity   69.8%;  Pred. No. 2.8e+03;
  Matches   30;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy    309 GCTGTGACCTTTGAGGTGGCTGAGGCCCCGGTGCCCAGCATAC 351
          | || | |||| | || ||||||||   ||||| |||| | |
Db      5 GATGGGCCCTTGGTGGAGGCTGAGGAGACGGTGACCAGGGTGC 47


RESULT 11
US-09-543-004-38
; Sequence 38, Application US/09543004
; Patent No. 6346249
; GENERAL INFORMATION:
;  APPLICANT:      Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt an
;  APPLICANT:  Lloyd J. Old
;  TITLE OF INVENTION:      A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THE
;  FILE REFERENCE:      LUD 5630.1
;  CURRENT APPLICATION NUMBER: US/09/543,004
;  CURRENT FILING DATE:  2000-04-04
;  PRIOR APPLICATION NUMBER:      09/425,638
;  PRIOR FILING DATE:      1999-10-22
;  NUMBER OF SEQ ID NOS:      129
; SEQ ID NO 38
;  LENGTH: 48
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
US-09-543-004-38

  Query Match             1.5%;  Score 22.2;  DB 4;  Length 48;
  Best Local Similarity   69.8%;  Pred. No. 2.8e+03;
  Matches   30;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy    309 GCTGTGACCTTTGAGGTGGCTGAGGCCCCGGTGCCCAGCATAC 351
          | || | |||| | || ||||||||   ||||| |||| | |
Db      5 GATGGGCCCTTGGTGGAGGCTGAGGAGACGGTGACCAGGGTGC 47


RESULT 12
US-07-609-716-22/c
; Sequence 22, Application US/07609716
; Patent No. 5514581
;  GENERAL INFORMATION:
;    APPLICANT:  Ferrari, Franco A.
;    APPLICANT:  Cappello, Joseph
;    TITLE OF INVENTION:  Functional Recombinantly Prepared
;    TITLE OF INVENTION:  Synthetic Protein Polymer
;    NUMBER OF SEQUENCES:  118
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/609,716
```

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;      FILING DATE:  06-NOV-1990
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rowland, Bertram I
;      REGISTRATION NUMBER:  20015
;      REFERENCE/DOCKET NUMBER:  A-55186-3/BIR
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-781-1989
;      TELEFAX:  415-398-3249
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  61 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-07-609-716-22

 Query Match             1.5%;  Score 22.2;  DB 1;  Length 61;
 Best Local Similarity   64.7%;  Pred. No. 3.2e+03;
 Matches   33;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy     229 GGCAGCTGCCTCCCCAGGACCAGCGGCGGCTGCTGCAGGGTTGCTGGGGCC 279
           | |||   || | ||||  ||||   ||||| |||||  | ||| ||  ||
Db      51 GCCAGAGCCCGCGCCAGCTCCAGAACCGGCTCCTGCACCGCTGCCGGCACC 1


RESULT 13
US-08-175-155-20/c
; Sequence 20, Application US/08175155
; Patent No. 5641648
;  GENERAL INFORMATION:
;    APPLICANT:  Ferrari, Franco A.
;    APPLICANT:  Cappello, Joseph
;    APPLICANT:  Crissman, John W.
;    APPLICANT:  Dorman, Mary A.
;    TITLE OF INVENTION:  Methods for Preparing Synthetic
;    TITLE OF INVENTION:  Repetitive DNA
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/175,155
;      FILING DATE:  29-DEC-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Rowland, Bertram I.
;      REGISTRATION NUMBER:  20015
;      REFERENCE/DOCKET NUMBER:  A-55186-5/BIR
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-781-1989
;      TELEFAX:  415-398-3249
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  61 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-175-155-20

  Query Match             1.5%;  Score 22.2;  DB 1;  Length 61;
  Best Local Similarity   64.7%;  Pred. No. 3.2e+03;
  Matches   33;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy     229 GGCAGCTGCCTCCCCAGGACCAGCGGCGGCTGCTGCAGGGTTGCTGGGGCC 279
           | |||   || | ||||  ||||   ||||| |||||  | ||| ||  ||
Db      51 GCCAGAGCCCGCGCCAGCTCCAGAACCGGCTCCTGCACCGCTGCCGGCACC 1


RESULT 14
US-08-477-509B-55/c
; Sequence 55, Application US/08477509B
; Patent No. 5770697
;  GENERAL INFORMATION:
;    APPLICANT:  Ferrari, Franco A
;    APPLICANT:  Cappello, Joseph
;    APPLICANT:  Crissman, John w
;    APPLICANT:  Dorman, Mary A
;    TITLE OF INVENTION:  No. 5770697el Peptides Comprising Repetitive
;    TITLE OF INVENTION:  Units of Amino Acids and DNA Sequences Encoding the Same
;    NUMBER OF SEQUENCES:  112
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,509B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/175,155
;      FILING DATE:  29-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/053,049
;      FILING DATE:  22-APR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/114,618
;      FILING DATE:  29-OCT-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 06/927,258
;      FILING DATE:  04-NOV-1986
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Trecartin, Richard F.
;      REGISTRATION NUMBER:  31,801
;      REFERENCE/DOCKET NUMBER:  A-55186-7/RFT/MTK
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-781-1989
;      TELEFAX:  415-398-3249
;  INFORMATION FOR SEQ ID NO:  55:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  61 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-477-509B-55

  Query Match             1.5%;  Score 22.2;  DB 1;  Length 61;
  Best Local Similarity   64.7%;  Pred. No. 3.2e+03;
  Matches   33;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy     229 GGCAGCTGCCTCCCCAGGACCAGCGGCGGCTGCTGCAGGGTTGCTGGGGCC 279
           | |||   || | ||||  ||||   ||||| |||||  | ||| ||  ||
Db      51 GCCAGAGCCCGCGCCAGCTCCAGAACCGGCTCCTGCACCGCTGCCGGCACC 1


RESULT 15
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```
US-08-707-237A-26/c
; Sequence 26, Application US/08707237A
; Patent No. 5830713
;  GENERAL INFORMATION:
;    APPLICANT:  Ferrari, Franco A.
;    APPLICANT:  Capello, Joseph
;    APPLICANT:  Crissman, John W.
;    APPLICANT:  Dorman, Mary A.
;    TITLE OF INVENTION:  METHODS FOR PREPARING SYNTHETIC
;    TITLE OF INVENTION:  REPETITIVE DNA
;    NUMBER OF SEQUENCES:  108
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Flehr, Hohbach, Test, Albritton & Herbert
;      STREET:  Four Embarcadero Center, Suite 3400
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94111-4187
;    COMPUTER READABLE FORM:
       MEDIUM TYPE:  Floppy disk
       COMPUTER:  IBM PC compatible
       OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/707,237A
;      FILING DATE:  03-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/175,155
;      FILING DATE:  29-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/053,049
;      FILING DATE:  22-APR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/609,716
;      FILING DATE:  06-NOV-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/269,429
;      FILING DATE:  09-NOV-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/114,618
;      FILING DATE:  29-OCT-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 06/927,258
;      FILING DATE:  04-NOV-1986
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Trecartin, Richard F.
;      REGISTRATION NUMBER:  31,801
       REFERENCE/DOCKET NUMBER:  A-55186-10/WHD
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 781-1989
;      TELEFAX:  (415) 398-3249
;      TELEX:  910 277299
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  61 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-707-237A-26

  Query Match             1.5%;  Score 22.2;  DB 2;  Length 61;
  Best Local Similarity   64.7%;  Pred. No. 3.2e+03;
  Matches   33;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy    229 GGCAGCTGCCTCCCCAGGACCAGCGGCGGCTGCTGCAGGGTTGCTGGGGCC 279
          | |||   || | ||||  ||||   ||||| |||||  | ||| ||  ||
Db     51 GCCAGAGCCCGCGCCAGCTCCAGAACCGGCTCCTGCACCGCTGCCGGCACC 1


Search completed: October 31, 2002, 23:18:35
Job time : 61 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: October 31, 2002, 21:51:41 ; Search time 57 Seconds
(without alignments)
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Title: US-09-919-197-3
Perfect score: 1456
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 310279 seqs, 166577418 residues

Total number of hits satisfying chosen parameters: 169348

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		26	1.8	73	10	US-09-466-320-16	Sequence 16, Appl
2		21	1.4	56	10	US-09-944-036-30	Sequence 30, Appl
3	c	21	1.4	64	10	US-09-919-580-637	Sequence 637, App
4	c	21	1.4	74	10	US-09-250-611-7	Sequence 7, Appli
5	c	20.6	1.4	70	10	US-09-878-574-8527	Sequence 8527, Ap
6		20.4	1.4	55	10	US-09-790-417-19	Sequence 19, Appl
7		20.4	1.4	67	10	US-09-878-574-5162	Sequence 5162, Ap
8	c	20.4	1.4	71	10	US-09-783-590-2509	Sequence 2509, Ap
9		20.4	1.4	73	10	US-09-783-590-3398	Sequence 3398, Ap
10		20.2	1.4	69	10	US-09-983-965-3899	Sequence 3899, Ap
11		20	1.4	51	10	US-09-874-547-8	Sequence 8, Appli
12	c	20	1.4	70	10	US-09-783-590-4790	Sequence 4790, Ap
13	c	20	1.4	75	10	US-09-864-761-28813	Sequence 28813, A
14	c	19.8	1.4	60	10	US-09-925-301-758	Sequence 758, App
15	c	19.8	1.4	60	10	US-09-975-408-68	Sequence 68, Appl
16	c	19.8	1.4	60	12	US-10-075-579-68	Sequence 68, Appl
17		19.8	1.4	70	10	US-09-822-250-30	Sequence 30, Appl
18		19.8	1.4	72	10	US-09-884-441-304	Sequence 304, App
19		19.8	1.4	73	12	US-10-108-280-18	Sequence 18, Appl
20		19.8	1.4	75	10	US-09-922-261-151	Sequence 151, App
21	c	19.6	1.3	48	10	US-09-810-502-29	Sequence 29, Appl
22		19.6	1.3	55	10	US-09-874-547-48	Sequence 48, Appl
23		19.6	1.3	56	9	US-09-144-886-39	Sequence 39, Appl
24		19.6	1.3	56	10	US-09-874-547-44	Sequence 44, Appl
25		19.6	1.3	56	10	US-09-988-899-49	Sequence 49, Appl
26	c	19.6	1.3	60	10	US-09-815-242-1130	Sequence 1130, Ap
27	c	19.6	1.3	71	10	US-09-783-590-5311	Sequence 5311, Ap
28		19.6	1.3	73	10	US-09-896-096A-4	Sequence 4, Appli
29		19.6	1.3	73	10	US-09-894-924-4	Sequence 4, Appli
30	c	19.4	1.3	55	10	US-09-920-300A-1151	Sequence 1151, Ap
31	c	19.4	1.3	55	12	US-10-033-528-1151	Sequence 1151, Ap
32		19.4	1.3	67	10	US-09-943-286-6	Sequence 6, Appli
33	c	19.2	1.3	26	10	US-09-780-172-13	Sequence 13, Appl
34	c	19.2	1.3	45	10	US-09-989-722-122	Sequence 122, App
35	c	19.2	1.3	45	10	US-09-989-723-122	Sequence 122, App
36	c	19.2	1.3	45	10	US-09-989-279-122	Sequence 122, App
37	c	19.2	1.3	45	10	US-09-989-727-122	Sequence 122, App
38	c	19.2	1.3	45	10	US-09-989-731-122	Sequence 122, App
39	c	19.2	1.3	45	10	US-09-989-732-122	Sequence 122, App
40	c	19.2	1.3	45	10	US-09-991-073-122	Sequence 122, App
41	c	19.2	1.3	45	10	US-09-990-442-122	Sequence 122, App
42	c	19.2	1.3	45	10	US-09-991-163-122	Sequence 122, App
43	c	19.2	1.3	45	10	US-09-993-604-122	Sequence 122, App
44	c	19.2	1.3	45	10	US-09-990-456-122	Sequence 122, App
45	c	19.2	1.3	45	10	US-09-989-721-122	Sequence 122, App

ALIGNMENTS

```
RESULT 1
US-09-466-320-16
; Sequence 16, Application US/09466320
; Patent No. US20020025939A1
; GENERAL INFORMATION:
;  APPLICANT: Iversen, Patrick
;  TITLE OF INVENTION: Chorionic Gonadotropin DNA Vaccines and
;  TITLE OF INVENTION: Methods
;  FILE REFERENCE: 0450-0026.30
;  CURRENT APPLICATION NUMBER: US/09/466,320
;  CURRENT FILING DATE: 1999-12-17
;  EARLIER APPLICATION NUMBER: US 60/112,910
;  EARLIER FILING DATE: 1998-12-18
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 73
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: coding sequence
US-09-466-320-16

  Query Match             1.8%;  Score 26;  DB 10;  Length 73;
  Best Local Similarity   62.1%;  Pred. No. 3.4e+02;
  Matches   41;  Conservative    0;  Mismatches   25;  Indels    0;  Gaps    0;

Qy    186 CTGGCCAAGACAGTGGCCTTCCTCAGGAACCTGCCATCCTTCTGGCAGCTGCCTCCCCAG 245
          | |  | ||||| |||    || | | |   | ||| || | |  |||  ||||||||||
Db      8 CCGTGCTAGACAATGGAGACCCGCTGAACAATACCACCCCTGTCACAGGGGCCTCCCCAG 67

Qy    246 GACCAG 251
          ||  ||
Db     68 GATAAG 73


RESULT 2
US-09-944-036-30
; Sequence 30, Application US/09944036
; Patent No. US20020055095A1
; GENERAL INFORMATION:
;  APPLICANT: YANG, Yeasing Y.
```

; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 56
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Capture
; OTHER INFORMATION: oligonucleotide
; 09-944-036-30

Query Match 1.4%; Score 21; DB 10; Length 56;
Best Local Similarity 62.3%; Pred. No. 7.6e+03;
Matches 33; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 1404 CTGAATTAAGTTATTGATTTTTGTAATAAAAGGTATGAAACACTAAAAAAAAA 1456
Db 2 CTGGAATAACTTCTGCTTCTATTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 54

RESULT 3
US-09-919-580-637/c
; Sequence 637, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 637
; LENGTH: 64
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 56
; OTHER INFORMATION: n = A,T,C or G
US-09-919-580-637

Query Match 1.4%; Score 21; DB 10; Length 64;
Best Local Similarity 65.2%; Pred. No. 8.2e+03;
Matches 30; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 1411 AAGTTATTGATTTTTGTAATAAAAGGTATGAAACACTAAAAAAAAA 1456
Db 64 AAGGCTTTNTTCTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 19

RESULT 4
US-09-250-611-7/c
; Sequence 7, Application US/09250611
; Patent No. US20020143161A1
; GENERAL INFORMATION:
; APPLICANT: Byrne, Jennifer A.
; APPLICANT: Basset, Paul
; TITLE OF INVENTION: Members of the D52 Gene Family
; FILE REFERENCE: 1383.0210001
; CURRENT APPLICATION NUMBER: US/09/250,611
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 74
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-250-611-7

Query Match 1.4%; Score 21; DB 10; Length 74;
Best Local Similarity 62.3%; Pred. No. 9e+03;
Matches 33; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 323 GGTGGCTGAGGCCCCGGTGCCCAGCATACTCAAGAAGATTCTGCTGGAGGAGC 375
Db 74 GGTCGCAGAGTTCCTCATGGCTGGCATACTTATTGAGTGGCGGATGGAGTAGC 22

RESULT 5
US-09-878-574-8527/c
; Sequence 8527, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 8527
; LENGTH: 70
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701101333H1
US-09-878-574-8527

Query Match 1.4%; Score 20.6; DB 10; Length 70;
Best Local Similarity 59.3%; Pred. No. 1.1e+04;
Matches 35; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 1355 AAGCTTAGGCTGCTTATTGGACCAGAAGTCCTATCGACTTTATACAGAACTGAATTAAG 1413
Db 68 AGGCTGCGGCTCATCATTCGACCGCCGGTCCAAGCGACCTTGCCCGGAATCGGTTCGAG 10

RESULT 6
US-09-790-417-19
; Sequence 19, Application US/09790417
; Patent No. US20010031470A1
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W.
; APPLICANT: Lewis, Martin K.
; APPLICANT: Lieppe, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B.
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Olson, Ryan J.
; APPLICANT: Wood, Keith W.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: Nucleic Acid Detection
; FILE REFERENCE: Pro-103 6868/75528
; CURRENT APPLICATION NUMBER: US/09/790,417
; CURRENT FILING DATE: 2001-02-22

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;  PRIOR APPLICATION NUMBER: 09/358,972
;  PRIOR FILING DATE: 1999-07-21
;  PRIOR APPLICATION NUMBER: 09/042,287
;  PRIOR FILING DATE: 1998-03-13
;  NUMBER OF SEQ ID NOS: 290
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 55
;   TYPE: DNA
;   ORGANISM: Cytomegalovirus
;   FEATURE:
;   OTHER INFORMATION: target for mutant cytomegalovirus
US-09-790-417-19

  Query Match             1.4%;  Score 20.4;  DB 10;  Length 55;
  Best Local Similarity   61.1%;  Pred. No. 1.1e+04;
  Matches   33;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy       8 CAGCCAACCAGGGGCCTGCCCATGCCAGGGAGCTGCAAGCCGCCCCGCCATTCT 61
           ||||    |  | || ||||  |  | | | || ||| ||||| ||| | | ||
         1 CAGCAGTGCGTGAGCTTGCCGTTCTCCGCGCGCGGCAGGCCGCGCCGGCGTGCT 54


RESULT 7
US-09-878-574-5162
; Sequence 5162, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
;  APPLICANT: Byrum, Joseph R.
;  APPLICANT:  La Rosa, Thomas J.
;  APPLICANT:  Thompson, Michael D.
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(15401)B
;  CURRENT APPLICATION NUMBER: US/09/878,574
;  CURRENT FILING DATE:  2001-12-21
;  PRIOR APPLICATION NUMBER: 09/333,535
;  PRIOR FILING DATE: 1999-06-14
;  NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 5162
;   LENGTH: 67
;   TYPE: DNA
;   ORGANISM: Glycine max
;   OTHER INFORMATION: Clone ID: LIB3028-022-Q1-B1-D9
US-09-878-574-5162

  Query Match             1.4%;  Score 20.4;  DB 10;  Length 67;
  Best Local Similarity   61.1%;  Pred. No. 1.3e+04;
  Matches   33;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy    1403 ACTGAATTAAGTTATTGATTTTTGTAATAAAAGGTATGAAACACTAAAAAAAAA 1456
           ||  || ||||| |    |||||||   ||||   |  | | |  |||||| ||
Db      11 ACCCAAATAAGTGAACTTTTTTTGTGCAAAAAAAAAAAATAAAAAAAAAACAA 64


RESULT 8
US-09-783-590-2509/c
; Sequence 2509, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
;  APPLICANT: Dillon, Patrick J.
;  APPLICANT:  Haseltine, William A.
;  APPLICANT:  Li, Haodong
;  APPLICANT:  Rosen, Craig A.
;  APPLICANT:  Ruben, Steven M.
;  TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
;  FILE REFERENCE: PO-16.2C1
;  CURRENT APPLICATION NUMBER: US/09/783,590
;  CURRENT FILING DATE:  2000-02-15
;  PRIOR APPLICATION NUMBER: 08/420,856
;  PRIOR FILING DATE: 1995-04-12
;  PRIOR APPLICATION NUMBER: 08/346,731
;  PRIOR FILING DATE: 1994-11-21
;  NUMBER OF SEQ ID NOS: 12485
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2509
;   LENGTH: 71
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (19)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (46)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (54)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (63)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (64)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (67)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc feature
;   LOCATION: (68)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-2509

  Query Match             1.4%;  Score 20.4;  DB 10;  Length 71;
  Best Local Similarity   56.6%;  Pred. No. 1.3e+04;
  Matches   30;  Conservative    0;  Mismatches   23;  Indels    0;  Gaps    0;

Qy    1404 CTGAATTAAGTTATTGATTTTTGTAATAAAAGGTATGAAACACTAAAAAAAAA 1456
           |  ||  ||   |    ||||| || ||||   |  ||| |  |||||| ||
Db      69 CNNAANNAAAAAAAAANTTTTTTTNAAAAAAAAAAAAAAAAAAAAAAAAAANAA 17


RESULT 9
US-09-783-590-3398
; Sequence 3398, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
;  APPLICANT: Dillon, Patrick J.
;  APPLICANT:  Haseltine, William A.
;  APPLICANT:  Li, Haodong
;  APPLICANT:  Rosen, Craig A.
;  APPLICANT:  Ruben, Steven M.
;  TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
;  FILE REFERENCE: PO-16.2C1
;  CURRENT APPLICATION NUMBER: US/09/783,590
;  CURRENT FILING DATE:  2000-02-15
;  PRIOR APPLICATION NUMBER: 08/420,856
;  PRIOR FILING DATE: 1995-04-12
;  PRIOR APPLICATION NUMBER: 08/346,731
;  PRIOR FILING DATE: 1994-11-21
;  NUMBER OF SEQ ID NOS: 12485
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3398
;   LENGTH: 73
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (32)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-3398

  Query Match             1.4%;  Score 20.4;  DB 10;  Length 73;
  Best Local Similarity   54.9%;  Pred. No. 1.3e+04;
  Matches   39;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;
```

```
Qy   1386 TATCGACTTTATACAGAACTGAATTAAGTTATTGATTTTTGTAATAAAAGGTATGAAACA 1445
          | || |  |  | || | | || ||  ||    || |    || ||||  .|  ||| |
Db      1 TTTCTAAGATGGAAAGTAATAAAATATATTTNAAATGTAAAAAAAAAAAAAAAAAAAAAA 60

Qy   1446 CTAAAAAAAAA 1456
          |||||||||
Db     61 AAAAAAAAAA 71
```

RESULT 10
US-09-983-965-3899
; Sequence 3899, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 3899
; LENGTH: 69
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 50-LIB3058-032-Q1-K1-E6
US-09-983-965-3899

Query Match 1.4%; Score 20.2; DB 10; Length 69;
Best Local Similarity 59.6%; Pred. No. 1.4e+04;
Matches 34; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

```
Qy   1394 TTATACAGAACTGAATTAAGTTATTGATTTTTGTAATAAAAGGTATGAAACACTAAA 1450
          | | | | ||  ||||||   |  ||||||  || ||||  ||  ||| |  |||
Db      1 TAAAAAAAAAAAAAATTAAAAAAACTATTTTTAAAAAAAAAAATACAAAAAAAAAA 57
```

RESULT 11
US-09-874-547-8
; Sequence 8, Application US/09874547
; Patent No. US20020058269A1
; GENERAL INFORMATION:
; APPLICANT: No, US20020058269A1k, Steffen
; APPLICANT: Kassner, Paul D.
; APPLICANT: Zyomyx, Inc.
; TITLE OF INVENTION: Screening of Phage Displayed Peptides
; TITLE OF INVENTION: Without Clearing of the Cell Culture
; FILE REFERENCE: 020144-001110US
; CURRENT APPLICATION NUMBER: US/09/874,547
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/209,503
; PRIOR FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primers for ScFv and Fab library generation (Table
; OTHER INFORMATION: I)- MHV-Back5
US-09-874-547-8

Query Match 1.4%; Score 20; DB 10; Length 51;
Best Local Similarity 72.2%; Pred. No. 1.4e+04;
Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```
Qy    415 CCCAGCCCTCCCTGGCTGCGGTGCAGTGGCTTCAAT 450
          |||||||  || |||| | ||| |||  ||  ||||
Db     14 CCCAGCCGGCCATGGCCGAGGTCCAGCTGCAACAAT 49
```

RESULT 12
US-09-783-590-4790/c
; Sequence 4790, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16.2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4790
; LENGTH: 70
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (46)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (59)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (61)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (62)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (68)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (70)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-4790

Query Match 1.4%; Score 20; DB 10; Length 70;
Best Local Similarity 60.4%; Pred. No. 1.7e+04;
Matches 29; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

```
Qy   1409 TTAAGTTATTGATTTTTGTAATAAAAGGTATGAAACACTAAAAAAAAAA 1456
          ||  |    |  |||||  || ||||   |  ||| |  |||||||||
Db     64 TTNNGNCCCTTTTTTTTTNAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 17
```

RESULT 13
US-09-864-761-28813/c
; Sequence 28813, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1

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;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 28813
;   LENGTH: 75
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC011815.2
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.57
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.49
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.51
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.58
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.93
;   OTHER INFORMATION: EST_HUMAN HIT: W45265.1, EVALUE 8.00e-35
;   OTHER INFORMATION: NT HIT: X94232.1, EVALUE 6.00e-35
US-09-864-761-28813

  Query Match             1.4%;  Score 20;  DB 10;  Length 75;
  Best Local Similarity   65.9%;  Pred. No. 1.7e+04;
  Matches   29;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy    249 CAGCGGCGGCTGCTGCAGGGTTGCTGGGGCCCCCTCTTCCTGCT 292
          | |||| ||||||||   |   ||| |  || |  ||||| |||
Db     60 CTGCGGGGGCTGCTGTTCGTGGGCTTGCTCCTCTGCTTCCGGCT 17


RESULT 14
US-09-925-301-758/c
; Sequence 758, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA106
;  CURRENT APPLICATION NUMBER: US/09/925,301
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05882
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 1694
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 758
;   LENGTH: 60
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (36)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (38)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (40)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (45)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (46)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-758

  Query Match             1.4%;  Score 19.8;  DB 10;  Length 60;
  Best Local Similarity   66.7%;  Pred. No. 1.7e+04;
  Matches   24;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy   1421 TTTTTGTAATAAAAGGTATGAAACACTAAAAAAAAA 1456
          ||||| ||| |||    |  | | |  |||||||||
Db     59 TTTTTTTAAAAAANNAAAANANANAAAAAAAAAAAA 24


RESULT 15
US-09-975-408-68/c
; Sequence 68, Application US/09975408
; Patent No. US20020150917A1
; GENERAL INFORMATION:
;  APPLICANT: Nanogen, Inc.
;  APPLICANT:  Weidenhammer, Elaine M.
;  APPLICANT:  Xu, Xiao
;  APPLICANT:  Kahl, Brenda F.
;  TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC
;  FILE REFERENCE: 267/174  Patrick S. Eagleman
;  CURRENT APPLICATION NUMBER: US/09/975,408
;  CURRENT FILING DATE:  2001-10-10
;  PRIOR APPLICATION NUMBER: 09/710,200
;  PRIOR FILING DATE: 2000-11-09
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
;   LENGTH: 60
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-975-408-68

  Query Match             1.4%;  Score 19.8;  DB 10;  Length 60;
  Best Local Similarity   63.8%;  Pred. No. 1.7e+04;
  Matches   30;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy   1410 TAAGTTATTGATTTTTGTAATAAAAGGTATGAAACACTAAAAAAAAA 1456
          | | | ||| |   ||| || ||||   |  ||| |  |||||||||
Db     48 TCACTGATTAAGCATTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2


Search completed: October 31, 2002, 23:19:53
Job time : 59 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: October 31, 2002, 21:09:57 ; Search time 1937 Seconds
(without alignments)
12173.789 Million cell updates/sec

Title: US-09-919-197-3
Perfect score: 1456
Sequence: 1 tgagcaccagccaaccaggg.....tatgaaacactaaaaaaaaa 1456

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

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Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
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Database : EST:*
1: em_estba:*
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3: em_estin:*
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8: em_htc:*
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17: gb_gss:*
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19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	32.4	2.2	34	9	AI221747	AI221747 qg93f02.x
c	2	29.8	2.0	62	17	B37921	B37921 HS-1046-A2-
	3	28.8	2.0	57	13	BI745330	BI745330 rk99b01.y
	4	28.2	1.9	52	9	AA782923	AA782923 ai62c05.s
	5	27.6	1.9	72	13	BI260363	BI260363 602969412
c	6	26.8	1.8	68	12	BF632727	BF632727 NF046A08D
c	7	26.6	1.8	53	14	H55352	H55352 CHR220291 C
	8	26.2	1.8	35	14	R37139	R37139 yf54g11.s1
	9	26.2	1.8	55	9	AI123105	AI123105 qa85b11.s
	10	26.2	1.8	60	14	R85541	R85541 yo38c03.s1
	11	25.8	1.8	47	14	H97244	H97244 yv98e05.s1
	12	25.6	1.8	46	9	AA916309	AA916309 on64a06.s
	13	25.4	1.7	61	12	BF581452	BF581452 602100856
c	14	25.4	1.7	63	10	AW333106	AW333106 S17D5 AGS
	15	25.2	1.7	47	14	N67514	N67514 za08g10.s1
	16	25.2	1.7	69	17	CNS02I4K	AL198461 Tetraodon
	17	25	1.7	65	17	AZ664880	AZ664880 1M0545H01
	18	25	1.7	74	9	AA574536	AA574536 vm29e03.r
c	19	24.8	1.7	46	9	AA853962	AA853962 aj51e02.s
c	20	24.8	1.7	61	9	AI144267	AI144267 qb59e02.x
c	21	24.8	1.7	67	10	AW633089	AW633089 bl03f09.x
	22	24.8	1.7	67	17	AZ397521	AZ397521 1M0162J05
	23	24.8	1.7	75	14	N68192	N68192 za11f07.s1
c	24	24.6	1.7	67	9	AI366713	AI366713 qy95b04.x
c	25	24.6	1.7	73	9	AA987684	AA987684 oq88a08.s
	26	24.4	1.7	70	14	BQ454399	BQ454399 ke04b11.y
c	27	24.2	1.7	63	9	AI274192	AI274192 ql46b08.x
	28	24.2	1.7	71	14	T25646	T25646 EST00515 Eq
c	29	24	1.6	64	9	AI448858	AI448858 ms45f07.x
c	30	24	1.6	69	17	CNS02I4K	AL198461 Tetraodon
c	31	24	1.6	72	9	AA809609	AA809609 nz17e02.s
c	32	23.8	1.6	59	10	AW168138	AW168138 xg60d06.x
	33	23.8	1.6	65	9	AI903143	AI903143 QV-BT022-
c	34	23.8	1.6	66	9	AI887645	AI887645 wm16d11.x
	35	23.8	1.6	67	2	HSM011809	Al046959 Homo sapi
	36	23.8	1.6	69	9	AL675639	AL675639 AL675639
c	37	23.8	1.6	70	9	AA785915	AA785915 i2h03a1.f
c	38	23.8	1.6	73	9	AI468883	AI468883 ti43e02.x
c	39	23.8	1.6	75	14	R52050	R52050 yj71d12.r1
c	40	23.6	1.6	65	9	AA599569	AA599569 ag08c08.s
	41	23.6	1.6	67	14	H47793	H47793 yp80e06.r1
c	42	23.6	1.6	70	9	AI250258	AI250258 qx03a04.x
	43	23.6	1.6	72	10	AV948273	AV948273 AV948273
c	44	23.6	1.6	72	14	BQ394194	BQ394194 NISC_ng07
c	45	23.4	1.6	53	9	AA632173	AA632173 np63a07.s

ALIGNMENTS

RESULT 1
AI221747/c
LOCUS AI221747 34 bp mRNA linear EST 30-NOV-1998
DEFINITION qg93f02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842747 3' similar to TR:Q15466 Q15466 NUCLEAR HORMONE RECEPTOR ;, mRNA sequence.
ACCESSION AI221747
VERSION AI221747.1 GI:3803950
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 34)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 990 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .34
/organism="Homo sapiens"

/db_xref="taxon:9606"
/clone="IMAGE:1842747"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 6 a 6 c 16 g 6 t
ORIGIN

Query Match 2.2%; Score 32.4; DB 9; Length 34;
Best Local Similarity 97.1%; Pred. No. 1.6e+03;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy    978 GCCTCCACCCTCAAGTCCATTCCGACCAGCCTGC 1011
          | ||||||||||||||||||||||||||||||||||
Db     34 GGCTCCACCCTCAAGTCCATTCCGACCAGCCTGC 1
```

RESULT 2
B37921/c
LOCUS B37921 62 bp DNA linear GSS 18-OCT-1997
DEFINITION HS-1046-A2-G04-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 829 Col=8 Row=M, DNA sequence.
ACCESSION B37921
VERSION B37921.1 GI:2542173
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 62)
AUTHORS Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S., Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.
TITLE Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence Tagged Connectors
JOURNAL Unpublished (1997)
COMMENT Contact: Mahairas GG; Zackrone KD, Hood L
University of Washington
Seattle, WA 98195, USA
Tel: (206) 616-8744
Fax: (206) 685-7301
Email: kzackron@u.washington.edu
Sequence Tagged Connector
Plate: CT 829 row: M column: 8
Class: BAC ends
High quality sequence stop: 62.
FEATURES Location/Qualifiers
source 1. .62
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=CT 829 Col=8 Row=M"
/clone_lib="CIT Human Genomic Sperm Library C"
/sex="M"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 15 a 15 c 19 g 12 t 1 others
ORIGIN

Query Match 2.0%; Score 29.8; DB 17; Length 62;
Best Local Similarity 70.2%; Pred. No. 7.5e+03;
Matches 40; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

```
Qy    565 TGCCCAAGGTCACCCAGCTAATAAGTGACAGTGCTGGGATTCATACCCAGGAAGCCT 621
          |||||||||||||||| || || | | ||| || |   | | |||||| || |
Db     60 TGCCCAAGGTCACCCAACTGGTATGTCTCTGACCTGCGACTGCGATCTAGGAAGTCT 4
```

RESULT 3
BI745330
LOCUS BI745330 57 bp mRNA linear EST 25-SEP-2001
DEFINITION rk99b01.y1 Meloidogyne javanica egg pAMP1 v6 Chiapelli McCarter Meloidogyne javanica cDNA 5', mRNA sequence.
ACCESSION BI745330
VERSION BI745330.1 GI:15767132
KEYWORDS EST.
SOURCE root-knot nematode.
ORGANISM Meloidogyne javanica
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
REFERENCE 1 (bases 1 to 57)
AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE The Washington Univ. Nematode EST Project, 1999
JOURNAL Unpublished (1999)
COMMENT Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu) at Washington University, St. Louis. DNA Sequencing by: Washington University Genome Sequencing Center St. Louis.
FEATURES Location/Qualifiers
source 1. .57
/organism="Meloidogyne javanica"
/db_xref="taxon:6303"
/clone_lib="Meloidogyne javanica egg pAMP1 v6 Chiapelli McCarter"
/dev_stage="enriched for eggs"
/lab_host="DH10B"
/note="Vector: pAMP1 (Gibco); The library was constructed by Brandi Chiapelli and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Nematodes were provided by Dr. David Bird of North Carolina State University."

BASE COUNT 26 a 1 c 4 g 26 t
ORIGIN

Query Match 2.0%; Score 28.8; DB 13; Length 57;
Best Local Similarity 75.0%; Pred. No. 1.3e+04;
Matches 36; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

```
Qy   1409 TTAAGTTATTGATTTTTGTAATAAAAGGTATGAAACACTAAAAAAAAA 1456
          || | ||||| |||||| |||||||| |  ||  | |  |||||||||
Db      7 TTGATTTATTTATTTTTTTAATAAAATGATTGTTAAAAAAAAAAAAA 54
```

RESULT 4
AA782923
LOCUS AA782923 52 bp mRNA linear EST 05-FEB-1998
DEFINITION ai62c05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375400 3' similar to gb:X57025_rna1 INSULIN-LIKE GROWTH FACTOR IA PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AA782923

```
VERSION     AA782923.1  GI:2842254
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 52)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
            , Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .52
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="1375400"
                     /clone_lib="Soares_testis_NHT"
                     /sex="male"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from mRNA obtained from Clontech Laboratories
                     , Inc., and primed with  a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTT 3']. 
                     Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization to Cot5, and was
                     constructed  by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT       20 a      9 c     14 g      9 t
ORIGIN

  Query Match             1.9%;  Score 28.2;  DB 9;  Length 52;
  Best Local Similarity   90.9%;  Pred. No. 1.9e+04;
  Matches   30;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     549 CAGAGATTAAGTGACTTGCCCAAGGTCACCCAG 581
           ||||| |||||||||||||||||| |||| |||
Db      20 CAGAGGTTAAGTGACTTGCCCAAGATCACACAG 52


RESULT 5
BI260363
LOCUS       BI260363                 72-bp    mRNA    linear   EST 17-JUL-2001
DEFINITION  602969412F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5108786 5',
            mRNA sequence.
ACCESSION   BI260363
VERSION     BI260363.1  GI:14818593
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 72)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Incyte Genomics, Inc.
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11263  row: h  column: 03
            High quality sequence stop: 72.
FEATURES             Location/Qualifiers
     source          1. .72
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5108786"
                     /clone_lib="NIH_MGC_12"
                     /tissue_type="cervical carcinoma cell line"
                     /lab_host="DH10B"
                     /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.4 kb. Library prepared by Life
                     Technologies."
BASE COUNT       44 a      4 c      6 g     18 t
ORIGIN

  Query Match             1.9%;  Score 27.6;  DB 13;  Length 72;
  Best Local Similarity   63.6%;  Pred. No. 2.7e+04;
  Matches   42;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy   1391 ACTTTATACAGAACTGAATTAAGTTATTGATTTTTGTAATAAAAGGTATGAAACACTAAA 1450
           ||  | |||||||| | |||     || ||| ||||   || ||||    |  |||    |||
Db      1 ACAGTTTACAGAAATAAATGTTTTTTTTGTTTTTCAGAAAAAAAAAAAAAAAAAACAAAAA 60

Qy   1451 AAAAAA 1456
           ||||||
Db     61 AAAAAA 66


RESULT 6
BF632727/c
LOCUS       BF632727                 68 bp    mRNA    linear   EST 19-DEC-2000
DEFINITION  NF046A08DT1F1065 Drought Medicago truncatula cDNA clone NF046A08DT
            5', mRNA sequence.
ACCESSION   BF632727
VERSION     BF632727.1  GI:11896885
KEYWORDS    EST.
SOURCE      barrel medic.
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 68)
  AUTHORS   Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
            Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
  TITLE     Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula drought library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: May GD
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 221 7391
            Fax: 580 221 7380
            Email: gdmay@noble.org
            Insert Length: 68   Std Error: 0.00
            Plate: 046  row: A  column: 08
            Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
     source          1. .68
                     /organism="Medicago truncatula"
                     /db_xref="taxon:3880"
                     /clone="NF046A08DT"
                     /clone_lib="Drought"
                     /tissue_type="Plantlets"
```

/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entire plantlets harvested in a series of days-post-watering timepoints. "
BASE COUNT 15 a 4 c 3 g 46 t
ORIGIN

Query Match 1.8%; Score 26.8; DB 12; Length 68;
Best Local Similarity 64.5%; Pred. No. 4.3e+04;
Matches 40; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

```
Qy   1395 TATACAGAACTGAATTAAGTTATTGATTTTTGTAATAAAAGGTATGAAACACTAAAAAAA 1454
          || |  ||| | ||||||||     || ||| |  |||||  |  ||| |  |||||||
Db     68 TAAAATGAAATAAATTAAGTCCGACATGTTTTTTTTAAAAAAAAAAAAAAAAAAAAAAAA 9

Qy   1455 AA 1456
          ||
Db      8 AA 7
```

[redacted]T 7
H55352/c
LOCUS H55352 53 bp mRNA linear EST 07-DEC-1995
DEFINITION CHR220291 Chromosome 22 exon Homo sapiens cDNA clone C22_364 5', mRNA sequence.
ACCESSION H55352
VERSION H55352.1 GI:1108218
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 53)
AUTHORS Trofatter,J.A., Long,K.R., Murrell,J.R., Stotler,C.J., Gusella,J.F. and Buckler,A.J.
TITLE An expression-independent catalog of genes from human chromosome 22
JOURNAL Genome Res. 5 (3), 214-224 (1995)
MEDLINE 96159527
COMMENT Contact: Buckler AJ
Molecular Neurogenetics Unit
Massachusetts General Hospital
Building 149, 13th St., Charlestown MA 02129
Tel: 6177249616
Fax: 6177265736
Email: buckler@helix.mgh.harvard.edu
Seq primer: T3.
FEATURES Location/Qualifiers
source 1. .53
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="C22_364"
/clone_lib="Chromosome 22 exon"
/lab_host="E. coli DH5a"
/note="Vector: pBluescriptIIKS+; Site_1: Sal I; Site_2: Bam HI (destroyed); Exons were isolated from human chromosome 22 specific cosmids using a modification of the method of exon amplification (Proc. Natl. Acad. Sci. USA 88:4005-4009, 1991). Amplified exons were digested with Sal I and Bgl II and subsequently cloned into pBluescriptIIKS+ at the Sal I and Bam HI sites."
BASE COUNT 12 a 16 c 10 g 15 t
ORIGIN

Query Match 1.8%; Score 26.6; DB 14; Length 53;
Best Local Similarity 71.4%; Pred. No. 4.7e+04;
Matches 35; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

```
Qy    535 AAGAAACTGAAGCCCAGAGATTAAGTGACTTGCCCAAGGTCACCCAGCT 583
          |||||||||| |||  ||| || ||||| |    |||||| |||   ||
Db     50 AAGAAACTGAGGCCTGGAGTTTGAGTGATTCCTTCAAGGTGACCACACT 2
```

RESULT 8

R37139
LOCUS R37139 35 bp mRNA linear EST 04-MAY-1995
DEFINITION yf54g11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:25970 3' similar to gb:X57025_rna1 INSULIN-LIKE GROWTH FACTOR IA PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION R37139
VERSION R37139.1 GI:794595
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 35)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1262
High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality
Insert Length: 1262 Std Error: 0.00
Seq primer: -21m13
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .35
/organism="Homo sapiens"
/db_xref="GDB:398317"
/db_xref="taxon:9606"
/clone="IMAGE:25970"
/clone_lib="Soares infant brain 1NIB"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: whole brain; Vector: Lafmid BA; Site_1: Not I; Site_2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 11 a 10 c 9 g 5 t
ORIGIN

Query Match 1.8%; Score 26.2; DB 14; Length 35;
Best Local Similarity 90.3%; Pred. No. 5.7e+04;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy    547 CCCAGAGATTAAGTGACTTGCCCAAGGTCAC 577
          | ||||| | ||||||||||||||||||||
Db      4 CACAGAGGTCAAGTGACTTGCCCAAGGTCAC 34
```

RESULT 9
AI123105
LOCUS AI123105 55 bp mRNA linear EST 05-OCT-1998
DEFINITION qa85b11.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1693533 3' similar to gb:X57025_rna1 INSULIN-LIKE GROWTH FACTOR IA PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AI123105
VERSION AI123105.1 GI:3538871
KEYWORDS EST.

```
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 55)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Insert Length: 1038   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1693533"
                     /clone_lib="Soares_fetal_heart_NbHH19W"
                     /sex="unknown"
                     /dev_stage="19 weeks"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by
                     M.Fatima Bonaldo. This library was constructed from the
                     same fetus as the fetal lung library, Soares fetal lung
                     NbHL19W."
BASE COUNT       18 a     11 c     17 g      9 t
ORIGIN

  Query Match             1.8%;  Score 26.2;  DB 9;  Length 55;
  Best Local Similarity   90.3%;  Pred. No. 6e+04;
  Matches   28;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     547 CCCAGAGATTAAGTGACTTGCCCAAGGTCAC 577
           | ||||| | ||||||||||||||||||||||
Db      24 CACAGAGGTCAAGTGACTTGCCCAAGGTCAC 54


RESULT 10
R85541
LOCUS       R85541                    60 bp    mRNA    linear   EST 14-AUG-1995
DEFINITION  yo38c03.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone
            IMAGE:180196 3' similar to gb:X57025_rna1 INSULIN-LIKE GROWTH
            FACTOR IA PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   R85541
VERSION     R85541.1  GI:943947
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 60)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
            ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
            Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
            ,R., Williamson,A., Wohldmann,P. and Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 2216
            High quality sequence starts: 1
            High quality sequence stops: 1
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Insert Length: 2216   Std Error: 0.00
            Seq primer: Promega -21m13
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .60
                     /organism="Homo sapiens"
                     /db_xref="GDB:3826840"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:180196"
                     /clone_lib="Soares adult brain N2b4HB55Y"
                     /sex="Male"
                     /dev_stage="55-year old"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: brain; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 53. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. The adult brain RNA was
                     provided by Dr. Donald H. Gilden. Tissue was acquired
                     17-18 hours after death which occurred in consequence of a
                     ruptured aortic aneurysm. RNA was prepared from a pool of
                     tissues representing the following areas of the brain:
                     frontal, parietal, temporal and occipital cortex from the
                     left and right hemispheres, subcortical white matter,
                     basal ganglia, thalamus, cerebellum, midbrain, pons and
                     medulla."
BASE COUNT       18 a     13 c     17 g     11 t      1 others
ORIGIN

  Query Match             1.8%;  Score 26.2;  DB 14;  Length 60;
  Best Local Similarity   90.3%;  Pred. No. 6.1e+04;
  Matches   28;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     547 CCCAGAGATTAAGTGACTTGCCCAAGGTCAC 577
           | ||||| | ||||||||||||||||||||||
Db      29 CACAGAGGTCAAGTGACTTGCCCAAGGTCAC 59


RESULT 11
H97244
LOCUS       H97244                    47 bp    mRNA    linear   EST 11-DEC-1995
DEFINITION  yv98e05.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:250784 3' similar to gb:X57025_rna1 INSULIN-LIKE GROWTH
            FACTOR IA PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   H97244
VERSION     H97244.1  GI:1114287
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
            ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
            Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
            ,R., Williamson,A., Wohldmann,P. and Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
```

```
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence starts: 1
            High quality sequence stops: 1
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Insert Length: 1257   Std Error: 0.00
            Seq primer: Promega -21ml3
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
     source           1. .47
                      /organism="Homo sapiens"
                      /db_xref="GDB:3868490"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:250784"
                      /clone_lib="Soares melanocyte 2NbHM"
                      /sex="Male"
                      /tissue_type="melanocyte"
                      /lab_host="DH10B (ampicillin resistant)"
                      /note="Vector: pT7T3D (Pharmacia) with a modified
                      polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                      was primed with a Not I - oligo(dT) primer [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTT 3'],
                      double-stranded cDNA was size selected, ligated to Eco RI
                      adapters (Pharmacia), digested with Not I and cloned into
                      the Not I and Eco RI sites of a modified pT7T3 vector
                      (Pharmacia). Library constructed by Bento Soares and
                      M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                      (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT       16 a      8 c     13 g      5 t      5 others
ORIGIN

  Query Match             1.8%;  Score 25.8;  DB 14;  Length 47;
  Best Local Similarity   84.4%;  Pred. No. 7.4e+04;
  Matches   27;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy     550 AGAGATTAAGTGACTTGCCCAAGGTCACCCAG 581
           |||| |||| |||||||||||||| ||  |||
Db      15 AGAGGTTAAGNGACTTGCCCAAGGNCANACAG 46


ULT 12
16309
OCUS        AA916309                 46 bp    mRNA    linear   EST 14-APR-1998
DEFINITION  on64a06.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
            IMAGE:1561426 3' similar to gb:X57025_rna1 INSULIN-LIKE GROWTH
            FACTOR IA PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   AA916309
VERSION     AA916309.1  GI:3055701
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES              Location/Qualifiers
```

```
     source           1. .46
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:1561426"
                      /clone_lib="Soares_NFL_T_GBC_S1"
                      /lab_host="DH10B"
                      /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                      a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                      Equal amounts of plasmid DNA from three normalized
                      libraries (fetal lung NbHL19W, testis NHT, and B-cell
                      NCI_CGAP_GCB1) were mixed, and ss circles were made in
                      vitro. Following HAP purification, this DNA was used as
                      tracer in a subtractive hybridization reaction. The driver
                      was PCR-amplified cDNAs from pools of 5,000 clones made
                      from the same 3 libraries. The pools consisted of
                      I.M.A.G.E. clones 297480-302087, 682632-687239,
                      726408-728711, and 729096-731399. Subtraction by Bento
                      Soares and M. Fatima Bonaldo. "
BASE COUNT       16 a     10 c     14 g      6 t
ORIGIN

  Query Match             1.8%;  Score 25.6;  DB 9;  Length 46;
  Best Local Similarity   87.5%;  Pred. No. 8.3e+04;
  Matches   28;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy     550 AGAGATTAAGTGACTTGCCCAAGGTCACCCAG 581
           |||| | |||||||||| |||||||||| |||
Db      15 AGAGGTGAAGTGACTTCCCCAAGGTCACACAG 46


RESULT 13
BF581452
LOCUS       BF581452                 61 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  602100856F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4224253 5',
            mRNA sequence.
ACCESSION   BF581452
VERSION     BF581452.1  GI:11655164
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 61)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9813  row: p  column: 14
            High quality sequence stop: 61.
FEATURES              Location/Qualifiers
     source           1. .61
                      /organism="Mus musculus"
                      /strain="FVB/N"
                      /db_xref="taxon:10090"
                      /clone="IMAGE:4224253"
                      /clone_lib="NCI_CGAP_Co24"
                      /lab_host="DH10B (T1 phage-resistant)"
                      /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
                      Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.6 kb. Constructed by Life
                      Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT       41 a      2 c      7 g     11 t
ORIGIN

  Query Match             1.7%;  Score 25.4;  DB 12;  Length 61;
```

```
  Best Local Similarity   68.6%;  Pred. No. 9.6e+04;
  Matches -  35;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy   1406 GAATTAAGTTATTGATTTTTGTAATAAAAGGTATGAAACACTAAAAAAAAA 1456
          ||||| | ||  ||| | || ||| ||||   |  ||| |  |||||||||
Db      2 GAATTTATTTGCTGAGTGTTCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 52


RESULT 14
AW333106/c
LOCUS       AW333106                 63 bp    mRNA    linear   EST 31-JAN-2000
DEFINITION  S17D5 AGS-1 Pneumocystis carinii f. sp. carinii cDNA 3', mRNA
            sequence.
ACCESSION   AW333106
VERSION     AW333106.1  GI:6829463
KEYWORDS    EST.
SOURCE      Pneumocystis carinii f. sp. carinii.
  ORGANISM  Pneumocystis carinii f. sp. carinii
            Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
            Pneumocystidaceae; Pneumocystis.
    RENCE   1  (bases 1 to 63)
    THORS   Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C., Edman
            ,J.C., Kovacs,J. and Cushion,M.
  TITLE     Expressed sequence tags from Pneumocystis carinii
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Staben C
            School of Biological Sciences
            University of Kentucky
            101 Morgan Building, University of Kentucky, Lexington, KY
            40506-0225, USA
            Tel: 606 257 2161
            Fax: 606 257 1717
            Email: staben@pop.uky.edu.
FEATURES             Location/Qualifiers
     source          1. .63
                     /organism="Pneumocystis carinii f. sp. carinii"
                     /db_xref="taxon:38081"
                     /clone_lib="AGS-1"
                     /lab_host="E. coli"
                     /note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
                     P. carinii organisms (3x10e9) from a single rat (99-1-6,
                     sacrificed on 3/17/99)  at Cincinnati VA facilities.
                     Trizol extracted RNA.  Oligo dT priming, standard
                     conditions described by  vendor, Stratagene. Further
                     details see www.uky.edu/Project/Pneumocystis/"
BASE COUNT       23 a      2 c      1 g     37 t
ORIGIN

  Query Match             1.7%;  Score 25.4;  DB 10;  Length 63;
  Best Local Similarity   74.4%;  Pred. No. 9.7e+04;
  Matches   32;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy   1414 TTATTGATTTTTGTAATAAAAGGTATGAAACACTAAAAAAAAA 1456
          | ||||||||||| |||||| |  |||  ||    |||||||||
Db     49 TAATTGATTTTTATAATAATATTTATATAATTAAAAAAAAAAA 7


RESULT 15
N67514
LOCUS       N67514                   47 bp    mRNA    linear   EST 08-MAR-1996
DEFINITION  za08g10.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:292002 3' similar to gb:X57025_rna1 INSULIN-LIKE GROWTH
            FACTOR IA PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   N67514
VERSION     N67514.1  GI:1219639
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
            ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
            Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
            ,R., Williamson,A., Wohldmann,P. and Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Seq primer: m13 -40 forward
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="Homo sapiens"
                     /db_xref="GDB:3885132"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:292002"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT       16 a      8 c     14 g      7 t      2 others
ORIGIN

  Query Match             1.7%;  Score 25.2;  DB 14;  Length 47;
  Best Local Similarity   84.4%;  Pred. No. 1.1e+05;
  Matches   27;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy    550 AGAGATTAAGTGACTTGCCCAAGGTCACCCAG 581
          |||| |||||||||| ||| |||||| || |||
Db     15 AGAGGTTAAGTGACNTGCGCAAGGTNACACAG 46


Search completed: October 31, 2002, 23:17:17
Job time : 1941 secs
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